79 158 237 316	390	25 450
TGC TAAA IGCT	N AAT	V GTA
PACCC PGACC PGCGP	M H Q M N ATG CAC CAA ATG AAT	V F A L L I V S F N H D V GTT TTT GCA CTT CTG ATA GTA TCT TTC AAC CAC GAT GTA
CGGC CGAAC GTTT	Q CAA	H CAC
CCAC GGAC AAAA	H	N AAC
ABAGP ABABG ABABC TTTAC	M ATG	F
TGCP TGGP TATP	CCA	S
ACAC TGCC TGTG	CTGA	V GTA
AGAC CTCC ACGG	TAAA	I ATA
GGGAA CCACT TGAC	CTCA	L
CTCA GTGA GTCG	SAAAT	L
ATCGAGIGGAA	BAGGG	A GCA
AAAGAAACGC	TGT	F
GAGA GAAA AGGT	GCTC	V GTT
AAGGAGGGAGGGAGGGAGGGAGGAGGAGGAGGAGGAGGA	ACTI	
GCTA ACAA CCATG	TTT	R AGG
AGCA CTAC ACTC	CTGI	F TTT
GCCGA CCGAA CTGG	TTTC	H CAC
TGCA GGTT AGGA	TTGC	M ATG
GTTTAGTCTGCAGCCGAGCAACCTAAAGGAAAAAATCGCTCAGGAAAGACACCTGCAGCAGCTCCACCGGCACCCTGC AATAGATGGGTTCCGACTACACAAGGGAGAAAACGCGGAGGTGACACTCTCCTGCCTG	TGAGGCAATTGCTTTTTAACTTGCTCTGTGAGGGAAATCTCATAAACTGACCA ATG CAC CAA ATG AAT	A K M H F R F GCT AAA ATG CAC TTT AGG TTT
GTTT AAT? CAA? GTT?	TGAC	A GCT

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T V ACT GTT	D N AT AAT
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105	125 750	145 810	165 870	185 930	205	225 1050	245 1110
S	V	E	D	E	D	Q	A
TCC	GTT	GAG	GAT	GAG	GAT	CAG	GCT
C TGT	E GAA	I ATT	P	I ATC	L TTA	P	P CCT
N	I	P	D	N	E	V	s
AAC	ATT	CCT	GAT	AAT	GAG	GTA	AGC
L TTG	H CAT	I ATA	F	${ m F}$	R AGA	G GGA	N AAC
N	F	L	A	F	V	M	D
AAC	TTC		GCA	TTT	GTC	ATG	GAC
K	L	S	S	D	V	D	N
AAA		TCT	AGT	GAT	GTG	GAC	AAT
Q	Q	R	D	N	I	S	S
CAG	CAG	AGA	GAC	AAT	ATA	TCA	
C	L	S	L	A	L	A	D
TGC	CTG	TCA	CTG	GCC	CTC	GCC	GAC
L	H	F	P	S	E	T	S
CTG	CAT	TTT		TCT	GAA	ACT	TCA
O CAA	E	Q CAG	I ATT	L	A GCA	L	I ATT
E	T	P	R	S	Y	Q	S
GAA	ACA		CGC	TCG	TAT	CAG	AGC
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T	I	N	A	CTC	D	S	I
ACA	ATC	AAT	GCA		GAT	AGC	ATA
A	V	I	A	S	T	S	S
GCT	GTG	ATT	GCA	TCC	ACT	TCA	TCC
ტტტ	D	D	S	N	R	K	S
ტტტ	GAT	GAT	AGT	AAT	AGG	AAG	TCA
I ATA	F TTT	L	e Gag	E GAA	T ACC	L	3 3 3 3
S AGC	E	V GTG	S	ე ეტე	R CGG	E	S TCT
IATC	I ATA	E	I ATA	V GTT	V GTT	R CGG	R AGG

Fig. 1B

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3/361 265 325 1350 345 1410 285 365 1470 1170 1230 302 1290 CIC FTTC H CAG GTG E \circ \gt TIG S TCC G GGA GTT GTT GAA Ы > \gt 臼 AGA GAT AAG Y TAT K AAA ACT \vdash 卍 × \Box GGC GAA ATT GGA GTA ATT Ö \triangleright 闰 Н Н Ŋ GTT GAG I ATT S TCT ATA PCCT > 闰 \vdash CCG K AAA D GAT TAT ATT S Д \succ Н ICC G GGG S TCC M ATG I ATT AAA S × AAC AAT TGC K AAA AAA L CTC C Z Z ¥ GAA ACC A GCT CAT N AAC F TTT Н 闰 田 I ATC TTA g GGC TACT GCC I ATC ᆸ ď CIC GAG GAG GAA AAC CCA Ы 闰 冝 闰 Д Z CAA GAT M ATG TAT I ATC ATT Ø О \succ \vdash ATA CCA GAT TCA GAA I ATT Ω Д ഗ 闰 ATA D GAT K AAA V GTG AAT CCT Д z TAT ACG P CAA CCA AAA \circ \succ ⊣ Д \bowtie TCT A GCC K AAG S TCT GGT AAT ß Ü Z GAC CAA GTG TIC TIG N AAT Ø \gt ഥ П \Box CAG L CTG H CAT GAT AAT Ы Ø \Box Z GAG CAA GAT AGT GTT 闰 \Box ₽ Ø Ø > TTT L TTA S AGC L TTG A GCT GAT Д

Fig. 10

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4/361 1890 505 525 1950 545 2010 1650 465 485 1830 265 AGA L $^{
m F}$ ACC T ACC TTG G GGA V GTA α H Ы GAT S AGT H I ATC ATC N AAT GTG CIC Н \gt CTG P P TAT ACC s TCT FTTT V GTG \succ ₽ ACA TACA CCA GCA TAC PCCA GTT TACT ø Н Д \succ \triangleright I ATC A GCC GGG GGG N AAT T ACA D GAC T ACA Ŋ Ŋ AAT R AGG D GAC CCA GTG Q CAG T ACC I ATT \gt Z Д T ACT D GAC N AAT Q CAA TCA TACC N AAT S AGT S TTAI ATC AAC G GGG V GTA EGAG GTG S AGC Z \gt I ATC AAT AAT Y TAT E GAA GTA A GCT D GAT Z Z \gt TTA I ATC GAA GAA TACA GAA L CTG N AAT 団 臼 冝 TAT V GTA I ATC TCA GGA TACT CAT CAA Ö Ŋ Ø 耳 AAT Q CAA ATT I ATA TACT LCTT D GAT K AAG Z \vdash AAC Γ TTG V GTT GTA GAT S TCC P F TTT Z \gt Ω GAA T ACA I ATC S AGC S AGT S AGT TTT P CCT 闰 Ŀ TAT TAT E GAT GGA R AGA GGA FTTT Ö \succ О Ö ACA GAG T ACA CTA Γ H CAT TAT GGA Ц Ü 闰 \succ AAG GCC S TCT K AAA CGA I ATT A GCC GAT × α Ø Ω Q CAG V GTG AGA AGC ACA TAT AGA TTT ഷ ß ₽ 엄 ഥ CTT AAG TACA AGA I ATC GCA GTT AGT Ø ĸ 民 > വ CAG AAA GAA ACT GAG A GCC GAA S TCT 口 Ø Η ା ロ

Fig. 1D

665 2130 645 2310 625 2250 685 705 725 605 2430 2550 2190 2490 ACG E GAG Q CAG S TCC N AAC A GCA GAT S AGT Ω AAT ATG T ACA C TGT R AGG N AAT CCT I ATT വ Σ S AGC AAT VGTG I ATT R AGG AAT I ATA GGT z Z I ATA CGT R AGA A GCA GTT GGC S TCG TACT Ŋ \gt പ്പ AAC AAA E GAG I ATA GCA L TTG T ACA V GTA ø Z ĸ ACC D GAC A GCA M ATG A GCA V GTC I ATA TTT⊢ Гъ A GCC CAT CAG S TCC Y TAT L CTA PCCT H CAT Ø 耳 C TGC I ATC I ATT E GAA GIC GTG GGG F TTT > ტ \gt I ATA g GGC S AGC GAC I ATC FTT D GAT M ATG Д L I ATC $\frac{1}{1}$ GTT S AGT C GTT I ATT \gt M ATG S TCC GIG TCA GTT GAA TCA E > 闰 Ŋ ß L L C TGC A GCA PCCT A GCT A GCT CGA α AAT E GAG K AAG Q CAG L TTG G GGG CCA GTT Д \triangleright Z L CTG S AGC V GTG AAC K AAA V GTG GAT TGG \Box 3 GAC A GCA CCC ATT E GAA CIT GTA GGT U \gt Н TACA V GTC AAT ATA C TGT I ATT S TCT S TCA Н Z T ACC GAC TAC I ATT GAA TIC AAA ACT × ⊣ 口 \succ \Box ഥ GCA GAC I ATC IATC P T ACC ATG AGA ø Σ α GAC GGA GAA AAT GTT CAT GCA Ø r 闰 > 耳 Д Z GAG T ACA L TTA LCTA A GCA I ATT S TCT 闰

5/361

Fig. 1E

6/361 825 2850 845 2610 865 745 765 802 2670 785 2730 2790 I ATA L TTA P CAC TIG ACT Ы Н 田 Σ GCC Q CAG CAG TACC TACC AGT Ø O വ Ω AAC TAC CAC CAA CCT Y TAT PCCT 耳 Д Z \succ ACT CIC ACC Q CAA V GTG TCT П Ц Н \vdash വ CIC G GGG S TCA $\frac{1}{1}$ TCA TCA Ы ø ß Ŋ GAA Q CAG GAA T ACA S TCT CAG Ø 闰 臼 \succ GCC I ATC CAC TTA H CAC R AGA CCA П Ø 田 Д D GAC TCA V GTG AGT CTT TCT ß ß വ \succ AGG G GGG TCG AAC TIC M ATG S AGC α ഗ \mathbf{z} ſΞι CAC C TGC K AAA AGA AAT S TCA 田 z α 召 AAC GAG CAC CAC AGT CTT 口 Ŋ 出 耳 Ŋ 口 Z Y TAT Y TAT CAT CAG CCA LCTT I ATT 王 Ø Д GTG CAG S TCC CAG CGG K AAA TCT α \circ \circ വ \gt AGC CAC s TCT AGA R CGG AGA പ്പ വ 出 Z 召 ATC GGC AAC GIC ACT TCC Ŋ \mathcal{O} ⊣ > ß z Н Q CAG GAC CCC CCA ATG TCA Ω α Д щ Σ ß GAG CTG CAG TCA AGG AAA × Ы 闰 α \circ ß ĹΤι I ATC GGG AAG K AAA ACT GTT × Ö വ ⊟ \gt ACA GAG GGC AGA GCT ø Д 闰 Д r വ് Н GTG GAA CCT R CGC H CAC N AAT R AGA > 闰 щ

1F Fig.

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3090 905 3150 925 TLL L CTG ഥ CIG GTC \gt GAC AGG α Д AGC C TGC വ TIC GAG 闰 ഥ GGA GAG 闰 ACG GAA 口 \vdash GGT C TGC Ċ LCIC CTG R AGA M ATG AGG പ്പ GAT GCT Ą Ü ø CCA Д $_{\rm ICI}$ വ \vdash GAT AGA О മ GGA Ü ഷ Ω Ö ACA Н r CIC Ω

945 3210 S AGT R AGG TAT بحر GAT Ω S TCT S TCT CCG Д S TCA PCCC L CCA Д CCA Д ATG Σ W TGG TGC O Q CAG GAC Ω S TCT CAC \mathbf{H} GGA Ö

965 3270 CAG Ø H CCA Д H CAT CAG Ø CAG Ø CAG Ø CCC Ľ CAA Ø ACG Н CCA Д TIC ĮΨ GAA 闰 GAA 闰 9999 Ö CCA Д ATG Σ AAC Z

7/361 3330 982 ACC Н TCC വ TTT ഥ AGT S AAG \bowtie AAG × AAG \bowtie GAA 闰 GGT Ŋ CC വ GAT \Box GCA Ø CCT Д CAG Ø GCT Ø GAC Ω GAT Д 闰 CTT Ы AGT വ

1005 3390 CTC Д CTG Ы TCT ß S TCA ACA ⊣ AGC ß ACC Н GAT \Box GGG Ŋ ACT Н GAC , D GAG 田 GAT Ω AAC Z, CCA · /中 ICC വ GAC 'n AAG × GGA Ö TTTſΞų

1025 3450 GAA 臼 S TCT TAT \succ TACC D GAC L S TCC PCCT P L TTA ᆸ R CGT CAG \circ TIC ഥ GIG \gt AGT വ AGC ß Σ GAA 臼 S TCG

3510 1045 AAA 노 GCC Ø CCA Д TTG Ы CCC വ GGA Ö AAG ¥ AGG ഷ CGC ヱ GAG · [五] CTG ᆸ S TCC AAC Z S TCC CGG വ് GAT \Box GIG \gt GAG 闰 AGT ß JGC Ö

Fig. 1G

				8/361
1065	1085 3630	1105 3690	1125 3750	1135 3783
P	` ™ TGG	L	I ATT	
N AAT	K AAA	V GTG	E GAG	
Q CAA	S TCA	N AAT	A GCA	
F TTT	S	D GAC	V GTG	
H	PCCT	F TTT	L	, :
T ACG	Q CAG	D GAT	E GAA	
S AGT	V GTG	D GAT	S AGT	
A GCC	1 S AGT	E	A GCC	
A ĞCA	S	E E	D GAT	:1
W TGG	H	Y TAT	M ATG	* TAG
A GCA	TACT	N AAT	L	S AGC
A GCG	G GGA	E GAA	E	CAG
V GTA	L CIT	ပ မ မ	H	A 100
	РССА	IATC	K AAA	V GT
Q CAG	P CCG	E GAG	GGG	D GAT
CCA	5 5 5 7	GAG	D GAT	Q CAA
Y TAC	C TGT	MATG	N AAT	CTT
GGT	N AAC	A GCC	L	LCTG
V GTG	T ACC	P	H CAC	K AAA
TACT	TACC	L CTG	N AAC	N -AAC
				*

3862 4099 4415 4020 4257 TTTTATTTTTTACTCCCATGACAGACATGTTTTTCCTAGTCGTGTAGAAACTAGCCACTGTTCAAATCTGATACACTA GAAGCATTATACAATTCTTAATTCCATTAAGTGATCCCACTTTTTTTCAATAACTTTTTAGAAATTAAGAATCATTAAA ATTGTTAAGCTATTTTATTGTTATTTTCTCTACTTCTACTAGCCCCCAATAGTTGAACTCTTATAGGAAAATCGAAAGA TATAGT CHAAGTTTTCAGGACTGAGAATATCTTGAAGGTTATTTATTAGATGACTATCTCAAATGAACTTTTTAT

Fig. 1H

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4889 4652 4810 4968 4731 5047 GTTCCGGAGAATATTTCTCTCTCACAATATTATTATCTTATAATTATGGTAAACAATAAATTTTATTCCATCCTTGTA TGGATAAAAACAGTTGTGTCAGTGTCTCTCTCTAAGGTAGTAAATATAATTGACTTATTCTGAACCCATTCTATTTGAA CTTGGTGAGAGAGATGCTTATTATGACTATTATCATTTCTGACCAAGCTTCTATTAATGTTATTTCTAATAATACACTA GTATGAAACATGCTCCAAGGAAATGGAATCTGTCCTTTAAATGGATAACAGTATGTGTTCTAATGGCATAAAATTAC AGACAATGATGAAAACAGAACTAAAGTCAATGTTTCCTGACTCCCAGGCCCCTACTATTCCAGGCCATCACTGGCCT

Fig. 11



158 237 316 GITIAGICIGCAGCCGAGCAGCTAAAGGAAAAAAATCGCICAGGAAAGAACACACACTGCAGAACTCCACCGGCACCTGC CAAACGCAAGGACTGGACTCCATGCCGAAGGTATCTGGAAGTCGTGACACGGTGTGTATAAAACAAAAGTTTGCGAGCT STTAATTGCTGTGTGTTATTAAGAGACGCTTTCAAGTTTCAAGTACCAAATGTAGCTTTACGTTGCAAAGGAAGT

10/361 45 25 65 390 450 85 AAT GCA GTA CGA ुंध ď ഷ GAT ATT GTT ტ Ω GTA CAC T ACT > H TCA ST AAC တ္ z Ω ט GGA CCT TGAGGCAATTGCTTTTGCTTTTAACTTGCTCTGTGAGGGAAATCTCATAAACTGACCA ATG 团 GTT $_{\rm ICI}$ N AAT > ഗ Z AGG GTA CCIഷ ሷ > CAG , L CTT ATA ___0 Y AAG CIG ः ু ध GAA L CTT GAG TTGCTT ц 臼 Ä TAT TTAGCA × ATT GLT > AGG FΩ GCT GAT GTT z ద TAC TTTט AGG AAA GTG ഷ TTG D GAT Ø AAT GAG 臼 Z Σ AAG TCA ß GGC CTA ט CIG AGA ᆸ

Fig. 2A

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11/361 205 245 185 930 225 1050 265 125 750 165 870 145 810 VGTT D GAT Q CAG E GAG E GAG D GAT A GCT LCTC I ATT I ATC L TTA PCCT E. GAA PCCA $\frac{1}{1}$ PCCT N AAT D GAT E GAG V GTA S AGC TACT I ATT PCCT TTT H CAT I ATA F TTT R AGA G GGA N AAC g GGC ഥ FTTT P D E D GAC F CTC A GCA MATG V GTT D GAC LCTT D GAT V GTG S SAGT N AAT P D GAC S TCC Q CAG N AAT S TCA R AGA I ATA S L L A GCC L A GCC D GAC AAC S TCA z H CAT P S TCT E GAA T ACT S TCA E GAA F TTT CHC L I ATT , Q CAG I ATT GAN E A GCA . L TTA R CGC S TCG Y TAT Q CAG S AGC LCTC P T ACA I ATA P Y TAC K AAG CIT P CCC CAA S TCT TACT K AAA ATA ი მმმ TACA A GCC E GAG L CTA AAT z H L CTA D GAC ATA H Y T ÀCT V GTT GGA ෆ TAT IATC L A GCA GAT S AGC I ATA N AAT Ω I ATT A GCA TACT S TCC S TCC S TCT S TCA AGG S TCA O CAA GAT S AGT N AAT K AAG D GAT ద gg g Q CAG E GAG GAA TACC L H H 臼 EGAG V GTG s TCT G GGG CGG E GAG S TCT മ്പ GTT R AGG F ITT I ATA I ATA V GTT R CGG E >

Fig. 2B

12/361 305 345 1410 365 1470 285 1230 325 1350 385 530 405 425 1650 590 F TTC H CAT Q CAG GTG GAA Q CAG AGA TTT \gt 冝 ഥ α TCC GGA V GTT GTT GAA CAC GAT GTT Ö > Ω Ŋ 闰 > 田 TAT R AGA K AAG D GAT AAA R AGA CTG GGT × Ы Ö GTA GAA I ATT GGA GTC I ATT CAT ACA > 闰 O \gt 出 Н ATT GAG ATA $\frac{1}{1}$ S TCT CCL GGA GCC 团 \vdash Д Ø Ŋ I ATT AAA GAT S TCC Y TAT A GCT CAT AAT \bowtie Д 耳 Z GGG S TCC AAA ATG I ATT ACT GTT CTT Ö 뇌 Σ \gt Ы Η AAT K AAA K AAA IGC CIC AAG TTT TTA Z \mathcal{O} Ы 니 ഥ ¥ CAT GCT F TTT T ACC AAC ACA ATC TGI ø 出 Z Η Ö Н GGC GCC I ATC TACT I ATC GAT GTT L TTA ø \mathcal{O} О \gt GAG GAG GAA AAC ATT CCA ATA TAT 闰 闰 闰 Д \mathbf{z} $\boldsymbol{\mathsf{H}}$ Н ⋈ GAT M ATG Y TAT ATC ATT GAA N AAT CCT О \mathbf{H} Н ρц 闰 CCA I ATT GAT TCA GAA GAT GGA AAC Д Ω Ŋ 闰 Д Ö Z GAT V GTG K AAA AAT GGG GAA CCT AAT Ω Д Ö 闰 Z Z ACG P CCC CAA CCA AAA GAA CTG TAT Н \circ Д ¥ 团 Ц \succ ggg K AAG 9999 ACA S TCT GGT AAT TTTØ Ö ſΞι ⊣ Z Ç AAT TIG GAC AAG GTG $_{
m F}$ ATT TCT ¥ Z > П О Н S CIG CAG CAT GAT AAT TAT GAT 田 Ы Ø Д Z \succ О GAT CAA AAG S AGT TACT GTT CTT TCT \Box Ø ß Ы \gt × s AGC $_{\mathrm{TTG}}$ GAC GAT ATA K AAA A GCT Ω Н Д

Fig. 2C



465 1770 F TTC CAC H PCCC P CCA N AAT D GAC N AAT I ATC GAT Д N AAT I ATC Q CAA V GTT T ACA F TTT H CAT K AAA V GTG T ACA S TCT

485 T ACC I ATC Y TAT A GCA G GGG PCCA S TCA N AAC N AAT GAA 团 S TCA I ATT GTA > F TTT E GAA Y TAT R CGA AGC S R AGA Q CAG

505 1890 L TTG I ATC T ACC $^{
m Y}$ T ACA V GTG Q CAA G GGG AAT z GAA 闰 GGA Ö LCTT GAT О PCCT GAT \Box ACA \vdash GCC Ø ACA Н GTT \gt T ACT

13/361 -525 1950 GGA Ö AAT Z S P CCA GAC Ω IATT ACC H GTA > TAT \succ ACA Н ACT Н ATA Н S TCC AGT വ GGA Ö CTA П ATT \vdash TTT ഥ S AGT 3AG 闰

545 2010 V GTA GTG > F TTT TACT IATC Q CAG S AGT GTG > GAA 闰 GAA 闰 CAT 出 GAT \Box TTT 压 ATC Н AGA ഷ CIC Ц GCC Ø TAT \succ ATC Н GCC ø

565 2070 T ACC L V GTG V GTT T ACA TACC AAT Z S AGC GTA \gt Γ CTG Q CAA K AAG CCG Д AGC ß GGA Ç GGA \mathcal{Q} GAT Ω AGA α GCA Ø GAA 闰

585 2130 ACG \vdash AAT Z AAT Z R CGT L TTG A GCA CCT Д GGG Ŋ ATA Н V GTT GTG \gt PCCT VGTT N AAC D GAC N AAT GAA 团 GAC Д ATT Н

Fig. 2D



605 625 2190 2250 GCA E GAG AGG N AAT 足 ATA G GGT AGA A GCA ഷ ACA V GTA Н GIC I ATA CAT A GCC 田 C TGC TTT ഥ GGC S AGC \mathcal{Q} AGT CIC Ŋ GAA E 闰 GCT A GCT Ø GGG N AAT Ü AAA V GTG \bowtie CCC GGT Д S TCT ACC GAC Н \Box AGA α GAA GAC 闰 Ω GCA I ATT

645 2310 D GAT M ATG S AGC V GTT N AAC T ACC H CAT I ATC D GAC $^{\rm C}$ S TCA R CGA PCCA D GAT I ATT I ATA TTC ഥ I ATC AAT Z E GAG

14/361 665 2370 685 CAG Ø ß CCT Н AAT > GGC S TCG AAA 囝 GAC Ø CAG \succ I ATT 回 I ATC ഥ GTT IATC TCA M ATG വ L C GAG × TGG 口 GAA LCTT ACA \gt \vdash TAC ¥ CCC T ACC GTT 耳 S TCT LCTA

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725 2550 N AAC TGT C R AGG TACT GCA Ø F TTT LCTA GTG \gt M ATG I ATT GTT \Rightarrow Γ L TTG V GTG A GCA TGT \mathcal{O} ATT \vdash GCA Ø GGA Ö L TTA

745 2610 CAC 田 Q CAG $^{
m Y}$ TACT S TCA GAA 团 A GCC GTG \triangleright AGG α C TGC AAC Z Y TAT S TCC R AGA ACT \vdash GAC \Box AAA ¥ AAG × GAG 回 R

2E Fig.

785 2730 825 2850 765 805 844 2907 864 2967 884 904 3027 3087 I ATA L TTA L ITG M ATG TACT Y TAT $_{
m TTT}$ ACC TACC A GCC D GAC S AGT D GAT PCCA LCTG \vdash CCT PCCT N AAC H Q CAG CAA D GAC S AGT Д T ACC GTG CIC Y TAT S TCT D GAC S AGC LCTT S TCA TTG LCTC S TCA Q CAA A GCC F GGA Ц ACA Q CAG E GAA G GGG Y TAT A GCA G GGA S TCT L TTA IATC H Q CAG R AGA P CCA E GAG GAA 臼 D GAC H Y TAC S TCT S AGT S TCA S AGT GGT N AAC ი მმმ S TCG FTTC CTT S AGC D GAC L CTG AAA H R AGG R AGA N AAT M ATG GGT L × CAC H E S TCA AGG S TCC S AGT R CGT 耳 足 ATT Q CAG Y TAT g GGC D GAT H CAT PCCA LCTT Н Q CAG R CGG V GTG LCIT K AAA I ATA S AGT S TCT H D GAC R CGG S AGC Q CAG N AAC R AGA PCCA ICC I ATC G GGC N AAC GGA s TCT K AAA s TCT ß PCCC D GAT M ATG S TCA V GTC R CGA L TTG CCA AGG L Q CAG S TCA E GAG S AGC FTTT CGA α α I ATC AAA ი მმ G GGG T ACT V GTT S AGT F TTT CCA G G G G R AGA T ACA PCCA AAA L TTG A GCT 노 CAC D GAC D GAT N AAT E GAA GTG P R AGA >

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Fig. 2F

16/361 1064 3507 1004 3387 1024 1044 3447 984 964 3267 944 3207 3147 PCCC K AAA GAA r CTC TACC Q CAG 团 S AGT r CTG A GCC N AAT TCTL CTG S TCC CAT GTC R AGG വ 耳 $^{
m Y}$ PCCA S TCT Ø $_{
m F}$ P CCA Y TAT AGG 姳 $_{
m F}$ L TTG TACC s TCA S AGT H CAT D GAT C TGC P D GAC TACA AAG 耳 Q CAG GAG S TCT ĸ 国 T ACG CIG G GGA S AGC K AAG Q CAG STCT GAG 闰 K AAG S TCC TACC വ AAG Q CAG CCG ACG × AGG CCT GAT Ø GAA P CCC ഷ Ы IGC S TCA Д 臼 CGC CCG GGG Ø GGT ഷ CAA Д CCC ט CIC r Ø Д Ы GAG TTA ACT ICC 口 z CTG Ë ACG ᆸ Н AGA ഗ Ц 召 CTG r CFC GAC ø GAT ᆸ CCA ATG CCA Д Ω Д Д Σ S TCC R CGT GAG A GCA F CCA GCT 闰 Д Ø N AAC Q CAG D GAT P CCT GAA M ATG GCA 闰 Ø s TCC N AAC F TTC Q CAG E GAA TGG CCA ⋈ R CGG VGTG P CCA A GCT а 966 c TGC ATT GAT S AGT s TCC D GAC Ω o CAG CCA AGA Д 24 V GTG AGC D GAC D GAT I ATT വ D GAC GGA Ċ ATG E GAG K AAG E GAG $_{
m F}$ Σ S TCT GAT Ω S AGT GAA GGA CTT M ATG 团 H CAC Ö IGC TCG FTT U S AGT N AAC വ GGA Ü

2G Fig.

CAA

CAT

AGT

ggg

GCA

 TGG

GCA

GCG

GTA

GGG

CAG

CCA

Y TAC

Ö

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Н

GGT

GIG

ACT

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1084	3627	1104	3687	1124	3747	1134	3780
×	TGG	ы	CIC	н	ATT		
×	AAA	>	GTG	田	GAG		
വ	TCA	Z	AAT		GCA		
ഗ	ICI	Д	GAC	>	GTG		
д	CCT	ഥ	TTT	ᄓ	CTG		
Ø	CAG		GAT	Ы	GAA		
>	GTG	О	GAT	ഗ	AGT		
ഗ	AGT	田	GAA	Ą	GCC		
ß	ICC	田	GAG	Ω	GAT		
	CAC		TAT	Σ	ATG	*	TAG
⊣	ACT	Z	AAT	П	CIC	യ	AGC
ტ	GGA ACT		GAA	团	GAA	Ø	CAG
ц	CTT	Д	CCI	H	CAC	ద	CGC
Д	CCA	Н	ATC	×	AAA	>	GIC
വ	SCG	田	GAG	Ċ	999	Д	GAT
ტ	999	田	GAG	Ω	GAT	Q	CAA
บ	TGT	Σ	ATG	Z	AAT	Ы	CTT
Z	AAC	Ą	<u> </u>	ᆸ	CIC	ы	CIG
₽	ACC	Д	CCA	H	CAC	×	AAA
₽	ACC	Ы	CTG	Z	AAC	z	AAC

4096 4254 4333 4412 4570 4491 TGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTCTGTGTATATTGAATATTAAATACTGTATTTCGTATGTACA ITTTATTTTTTTCTCCCATGACAGACATGTTTTTCCTAGTCGTGTAGAAACTAGCCACTGTTCAAATCTGATACACTA ITCAACCACAAAGTGTAAAGGCACTGCTTAGATTAGTTTTGTTGGGGAAGAATTATTATGTTGTATGAACAACCCCACT SAAGCATTATACAATTCTTAATTCCATTAAGTGATCCCACTTTTTTTCAATAACTTTTAGAAATTAAGAATCATTAAA **ATTGTTAAGCTATTTTTTTTTTTTTTTTCTCTACTTTCTACTAGCCCCCAATAGTTGAACTCTTATAGGAAAATCGAAAGA** STICCGGAGAATATITCICICACAATATIATTATCTACTTATAATTATGGTAAACAATAAATTTTATTCCATCCTTGTA GTATGAAACATGCTCCAAGGAAATGGAATCTGTCCTTTAAATGGATAACAGTATGTGTTCTAATGGCATAAATATTAC AGACAATGATGAAAACAGAACTAAAGTCAATGTTTCCTGACTCCCAGGCCCCTACTATTCCAGGCCATCACACTGGCCT TGGATAAAAACAGTTGTGTCAGTGTCTCTCCTAAGGTAGTAAATATAATTGACTTATTCTGAACCCATTCTATTTGAA

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Fig. 21

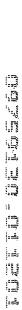
T416	1651 GAAAAGAGATCTGAGTATAGTTTGACTGTAATCGCTGAGGACAGGGGGAC 1700
AL137471	
T416	
AI,137471	248 TTCTAGGAAGTTCCATAACTACATATGTAACCATTGACCCATCTAATGGA 297

FIG. 4A

POZECIOL OLINO

T416	1951 GCCATCTATGCCCTCAGAATCTTTGATCATGAAGAAGTGAGTCAGATCAC 2000
AL137471	298 GCCATCTATGCCCTCAGAATCTTTGATCATGAAGAAGTGAGTCAGATCAGAAGAAGAAGTGAGTG
T416	2001 TTTTGTGGTAGAAGCAAGAGAGAGGGAAGCCCGAAGCAACTGGTAAGCA 2050
AL137471	
T416	2051 ATACCACAGTTGTGCTCACCATCATTGACGAAAATGACAACGTTCCTGTG 2100
AL137471	
T416	2101 GTTATAGGGCCTGCATTGCGTAATAATACGGCAGAAATCACCATTCCCAA 2150
AL137471	
T416	
AL137471	
T416	
AL137471	

FIG. 41



T416	2251	GAGAATATCTTCATAATTGATCCACGATCATGTGACATCCATACCAACGT 2300
AL137471	598	
T416	2301	TAGCATGGATTCTGTTCCCTACACAGAATGGGAGCTGTCAGTTATCATTC 2350
AL137471	648	
T416	2351	AGGACAAAGGCAATCCTCAGCTACATACCAAAGTCCTTCTGAAGTGCATG 2400
AL137471	698	
T416	2401	ATCTTTGAATATGCAGAGTCGGTGACAAGTACAGCAATGACTTCAGTAAG 2450
AL137471	748	
T416	2451	CCAGGCATCCTTGGATGTCTCCATGATAATAATTATTTCCTTAGGAGCAA 2500
AL137471	798	
T416	2501	TITGTGCAGTGTTGCTGGTTATTATGGTGCTATTTGCAACTAGGTGTAAC 2550
AL137471	848	

FIG. 40

normal so on thos

T416	2551	CGCGAGAAGAAGACACTAGATCCTATAACTGCAGGGTGGCCGAATCAAC 2600
AL137471	8 9 8	
T416	2601	TTACCAGCACCACCAAAAAGGCCATCCCGGCAGATTCACAAAGGGGACA 2650
AL137471	948	
T416	2651	TCACATTGGTGCCTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC 2700
AL137471	966	
T416	2701	AGATCGTCTCCATCTTCATCTCCTACCTTAGAAAGAGGGCAGATGGGCAG 2750
AL137471	1048	
T416	2751	CCGGCAGAGTCACAACAGTCACCAGTCACTCAACAGTTTGGTGACAATCT 2800
AL137471	1098	
T416	2801	CATCAAACCACGTGCCAGAGAATTTCTCATTAGAACTCACCCACGCCACT 2850
AL137471	1148	CATCAAACCACGTGCCAGAGAATTTCTCATTAGAACTCACCCACGCCACT 1197

FIG. 4D



T416	2851 CCTGCTGTTGAGCAGGTCTCTCTCTTTCAATGCTTCACCAGGGGCA 2900
AL137471	
T416	2901 ATATCAGCCAAGACCAAGTTTTCGAGGAAACAAATATTCCAGGAGCTACA 2950
AL137471	
T416	
AL137471	
T416	3001 GGTGACAGTGAGGCAGGAGACAGTGATTATGATTTGGGGCGAGATTCTCC 3050
AL137471	
T416	3051 AATAGATAGGCTGCTGGGTGAAGGATTCAGCGACCTGTTTCTCACAGATG 3100
AL137471	
T416	3101 GAAGAATTCCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCTG 3150
AL137471	

FIG. 41

COPEDITO DI LECE

T416	3151 GGACACTCTGACCAGTGCTGGATGCCACCACTGCCCTCACCGTCTTCTGA 3200
AL137471	
T416	3201 TTATAGGAGTAACATGTTCATTCCAGGGGAAGAATTCCCAACGCAACCCC 3250
AL137471	
T416	3251 AGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT 3300
AL137471	
T416	3301 TCCGGTGAAAAAAAAAGAAGAGTTTTTCCACCTTTGGAAAGGACTCCCCAAA 3350
AL137471	
T416	3351 CGATGAGGACACTGGGGATACCAGCACATCATCTCTCTCT
AL137471	
T416	3401 GCAGTGTTCCAGCGTCTCTTACCGCCTTCCCTGGACACCTATTCTGAA 3450
AL137471	1748 GCAGTGTTTCCAGCGTCTCTTACCGCCTTCCCTGGACACCTATTCTGAA 1797

FIG. 4F



T416	3451 T	GCAGGAAGGGACCCTT 3500
AL137471		
T416	3501 G	GCGGCATGGGCAGCCA 3550
AL137471		
T416	3551 G	GCCGCCACTTGGAACT 3600
AL137471		
T416	3601 C	CAGCCATGGAGGAGAT 3650
AL137471		
T416	3651 C	GTGCTCAACCACCTCA 3700
AL137471		
T416	3701 ATGATGGGAAACACGAACTCATGGATGCCAGTGAACTGGTGGCAGAGATT	ACTGGTGGCAGAGATT 3750
AL137471	2048 ATGATGGGAAACACGAACTCATGGATGCCAGTGAACTGGTGGCAGAGTT	

FIG. 46

COPETAL DEFE

T416	3751 AACAAACTGCTTCAAGATGTCCGCCAGAGCTAGGAGATTTTAGCGAAGCA 3800
AL137471	
T416	
AL137471	
T416	
AL137471	2198 CCCTGAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC 2247
T416	3901 TGTGTATATTGAATATTAAATACTGTATTTTCGTATGTACACAATGCAAG 3950
AL137471	
T416	3951 TGTGATTATTTTAATTTTTAAAATACATTTGTACCTTATATTTA 4000
AL137471	2298 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 4F

45	50	9 0	ე დ	142	148	192	193	242	242
ATGCACCAAATGAATGCTAAAATGCACTTTAGGTTTGTTTTTGCA		CTT(51 CTTGTTCATTTCAGGGATTGTCAGGAGGTGGCCACTGTCATGGTGAA	93 ATACAGGATTTATGAGGAACAGAGGGTTGGATCAGTAATTGCAAGACTAT	TCCAAGTGACAGAGGAAGTGCCGTCT	143 CAGAGGATGTGTTTTTTTTTGAAGCTTCCTAATCCTTCTACTGTT 	ggg.	193 CGATTTCGAGCCATGCAGAGGGAAATTCTCCTCTACTTGTAGTAAACGA	194 CCTTCCAGATTC.TGCAGCTGCCTCAGGCACTGCCGGTTCAGATGAACTC
T416	m-PC	T416	m - FC	T416	m-PC	T416	m-PC	T416	m-PC

FIG. 5A

COVECTUC CTTECT

T416	243 (GGATAATGGGGAAATCAGCATAGGGGCTACAATTGACCGTGAACAACTGT	292
m-PC	243 '		292
T416	293 (GCCAGAAAAACTTGAACTGTTCCATAGAGTTTGATGTGATCACTCTACCC	342
m-PC	293 (GTCGGCAGGAAGATCCCTGTCTGGTGTCATTTGACGTGCTTGCC	336
T416	343	ACA.GAGCATCTGCAGCTTTTCCATATTGAAGTTGAAGTGCTGGATATTA	391
m-PC	337		385
T416	392	CTCTCATACCTAI	441
m-PC	386		435
)
T416	442	GAGAGTGCAGTTGGGACTCGCATTCCCCTGGACAGTGCATTTGATCC	491
m-PC	436 (485

FIG. SE

T416		541
m-PC		535
T416		591
m-PC	TTGTGG	585
T416	592 CTCATAGTGATCAGAGTTAGATCGGGAGCTGAAGTCAAGCTACGAGCT	641
m-PC	11	635
T416	. 642 TCAGCTCACTCAGAC.ATGGGAGTACCTCAGAGGTCTGGCTCATCC	069
m-PC	636 GGTGCTGACCGCCTATGACAATGGGAAT.CCCCCTAAGTCAGGAATCAGC	684
Т416	691 ATACTAAAAATAAGCATTTCAGACTCCAATGACAACAGGCCTGCTTTTGA	740
m-PC	685 GIGGICAAIGICCTGGACTCCAAIGACAATAGICCAGIGITIGC	734

FIG. 50

FINE FR. OF FREE FREE

T416	741 GCAGCAATCTTATATA	CAGCAATCTTATATAATACAACTCTTAGAAAACTCCCCGGTTGGCACTT	790
m-PC	 		784
T416	791 TGCTCTTAGATCTGAA		840
m-PC			834
T416	841 ATTGTATATTCCTTCA	TTGTATATTCCTTCAGCAGTCATGTGTCTCCCAAAATTATGGAGACTTT	890
m-PC			884
T416	891 TAAAATTGATTCTGAA	. TAAAATTGATTCTGAAAGGACATTTGACTCTTTTCAAGCAAG	940
m-PC	885 TGGCATAGATGCCAAG		934
T416	941 ATGAAATCACCAAATC		066
m-PC	935 ACGAGAAGAACCCTGC		984

FIG. 51

T416	991	CCAAATTCAATCCCAGCCCATTGCAAATTATAATTAAGGTTGTGGATGT 1040
m-PC	985	
T416	1041	ACCTGAAAT
m-PC	1035	CAATGACAATGCCCCAAGCATCCTCATCACGTGGGCCTCC 1074
T416	1091	NTCTTAT
m-PC	1075	CAGACGTCGCTGGTGTCAGAAGATCTTCCCAGGGATAGCTTCATTGCC 1122
T416	1141	
m-PC	1123	
T416	1191	TAAGCTTCATGGACATGGTCACTTTAAACTTCAGAAGACATATGAAA 1237
m-PC	1173	TIGGCIGAATCAAGAGCIGGGCCACTICAGACTGAAAAGGACTAACGGCA 1222

FIG. 51

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T416	1238	ACAATTATTTAATCTTAACTAATGCCACACTGGATAGAGAAAAGAGATCT 1287
m-PC	1223	
T416	1288 (GAGTATAGTTTGACTGTAATCGCTGAGGACAGGGGGACACCCAGTCTC 1335
m-PC	1273	ATATATACTCTCACTGTTTTGCCCAAGAC.CAAGGAC.CCCAGCCCTTA 1320
T416	1336	TCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCAATGACAATCC 1385
m-PC	1321	II
T416	1386 /	ACCCCACTTCCAGAGAGCCGATATGAATTTGTAATTTCAGAAAATAACT 1435
m-PC	1371 (TCTCC
T416	1436 (CACCAGGGCATATATCACCACTGTTACAGCCACAGATCCTGATCTTGGA 1485
m-PC	1421 (_ 🔾

FIG. 51

COVERTO CITER

T416	. 71
m-PC	
T416	
m-PC	 TCAGCCTGTGC

FIG. 50

SOPESIES CHIEST

T416	1705	GAAAATGACAACGTTCCTGTGGTTATAGGGCC1736
m-PC	1717	
T416	1737	AAT.?
m-PC	1767	
T416	1772	
m-PC	1817	CACCAAAGGCTACCCACAGCCCCTGGTCTTTCCTTTTGTTAACAATCGTG 1866
T416	1813	GCAATTGACAGAGACTCTGGTGTAATGCTGAACTCAGCTGCGCCATAGT 1862
m-PC	1867	
T416	1863	AGCAGGTAATGAGGAGAATATCTTCATAATTGATCCACGATCATGTGACA 1912
m-PC	1917	

FIG. 5B

r416	1913 TCCATACCAACGTTAGC.ATGGATTCTGTTCCCTACACAGAATGG 1957	
n-PC		
r416		
n-PC		
ľ416		
n-PC	11	
F416		
n-PC		
F416		
n-PC	2155 TTGATCTGCCTGTACTGCTGGCCATCTTTGGATTGCTCTTAGCCCT 2204	

FIG. 5

r416	2157 A	ATTTGCAACTAGGTGTAACCGCGAGAAGAAAGACACTAGATCCTATAACT 2206
n-PC	2205 G	
r416	2207 G	GCAGGGTGGCCGAATCAACTTACCAGCACCACCAAAAAGGCCATCCCGG 2256
n-PC	2255 G	
ľ416	2257 (TTGGTGCCTACCATA
n-PC	2305 0	
r416	2307 G	ACAGAT
n-PC	2353 G	
. 416	2351 .	
n-PC	2402 A	

FIG. 53

T416	GTCACTCAACAGTTTGGTGACAATCTCATC	
m-PC		
T416	2438TGCCAGAGAATTTCT.CATTAGAAC.TCACCCACGCC 2472	
m-PC	AGAGCC.	
T416		
m-PC		
T416	TCAGCCAAGACCAAGTTTTCG	
m-PC		
T416	2559 ATATTCCAGGAGCTACAGATA.TGCCCTTCAAGACATGGACAAATTTAGC 2607	
m-PC		

FIG. 5K

1416	2608 TTGAAAGACAGTGGCCGTGGTGACAGTGAGGCAGGAGACAG.TGATTA 2654	
ı-PC		
.416		
ı-PC		
1416		
ı-PC		
1416		
n-PC	II I CTCTCCTC	
1416		
n-PC	2887 TCCCAGCTGCTGCTGCACCAGGCCCAATTCCAGCCCAAACCAAA 2936	

FIG. 51

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T416	2843 TCATTCCAGGGAAGAATTCCCAACGCAACCCCAGCAGCAGCATC 2887
m-PC	
T416	2888 . CACATCAGAGTC.TTGAGGATGACGCTCAGCCTGCAGATTCCGGTGAAA 2935
m-PC	2985 TACCATCCCAGACACAGGGCCTTG.TAGGCCTCAAGCCT.AGTGGCCA 3032
T416	GAGTTTTCCACCTTTGGAAAGGACTCCCCAAACGAT
m-PC	
T416	
m-PC	
T416	3035 TCCAGCGTCTTACCGCCTTCCCTGGACACCTATTCTGAATGCAGTG 3082
m-PC	3122 TGGACCCTAATACAGGTCTAGCCCTGGACAAGCTGAGTCCGCCTGACCCA 3171

FIG. SM

T416	G.GTCCAACTCCCTGGAG
m-PC	
T416	
m-PC	
T416	ATCCCACCACCAAC
m-PC	
T416	3232 AGIGIGCAGCCTICTTCAAATGGCTGCCAGCCATGGAGGAGATCCCT 3279
m-PC	
T416	3280GAAAATTATGAGGAAGATGATTTTTGACAATGTGCT.CAACCACC 3322
m-PC	

FIG. SN

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m-PC		50
T416		48
m-PC	\sim	86
T416	::	8
m-PC	LATGASALIHVEIQVLDINDHQPQFPKDEQE	146
T416	:	148
m-PC	/GP	196
T416	·· :- ·: ::	198
m-PC	197 VVVKELDRELHSYFDLVLTAYDNGNPPKSGISVVKVNVLDSNDNSPVFAE	246
T416	: : :: : :: :	248

FIG. 6A

m-PC	247 SSLALEIPEDTVPGTLLINLTATDPDQGPNGEVEFFFGKHVSPEVMNTFG	296
T416	::: ·· :. : .: : : 249 QSYIIQLLENSPVGTLLLDLNATDPDEGANGKIVYSFSSHVSPKIMETFK	298
m-PC	297 IDAKTGQIILRQALDYEKNPAYEVDVQARDLGPNSIPGHCKVLIKVLDVN	346
T416	: · · · ·	348
m-PC	347 DNAPSILITWASQTSLVSEDLPRDSFIALVSANDLDSGNNGLVHCW	392
T416		398
m-PC		442
T416		447
m-PC		492
T416	448 VKHFTVQINDINDNPPHFQRSRYEFVISENNSPGAYITTVTATDPDLGEN	497

FIG. 6B

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m-PC	RIKDSPVSHLVIIDF	537
T416	· · : :	547
m-PC	538 EDRGOP.QLASSISVWVSLLDANDNAPEVIQPVLSEGKATLSVLVNASTG	586
T416		597
m-PC	587 HLLLPIENPSGMDPAGTGIPPKATHSPWSFLLLTIVARDADSGANGELFY	636
T416	.	618
m-PC		989
T416	· 4	299
m - PC	FVTSVDHLRDSAHEPGVLSTPALALICLAVLLAIFGLLL	733
T416	89	717

FIG. 6C

m-PC	734 ALFVSICRTERKDNRAYNCREAESSYRHQPKRPQKHIQKADIHLVPVLRA	783
T416	· : ·	767
m-PC	784 HENETDEVRPSHKDTSKETLMEAGWDSCLEAPFHLTPTLYRTLRNQGN	831
T416		817
m-PC	832 QGELAESQEVLQDTFNFLFNHPRQRNASRENLNLPESPPAVRQPLLRPLK	881
T416	· · · · · · · · · ·	867
m-PC	882 VPGSPIARATGDQDKEEAPQSPPASSATLRRQRNFNGKVSPRGESGPHQI	931
T416		913
m-PC	932 LRSLVRLSVAAFAERNPVEEPAGDSPPVQQISQLLSLLHQGQFQPKPNHR	981
T416		963

FIG. 61

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m-PC	982 G	GNKYLAKPGGSSRGTIPDTEGLVGL.KPSGQAEPDLEEGPPSPEEDLSVK 1030
T416	964 H	HQSLEDDAQPADSGEKKKSFSTFGKDSPNDEDTGDTSTSSLLSEMSSVFQ 1013
m-PC	1031 R	RLLEEELSSLLDPNTGLALDKLSPPDPAWMARLSLPLTTNYRDNLSS 1077
T416	1014 R	
m-PC	1078 P	PDATTSEEPRTFQTFGKTVGPGPELSPTGTRLASTFVSEMSSLLEMLLGQ 1127
T416	1064 N	NPTINCGPPLGTHSSVQPSSKWLPAMEEIPENYEEDDFDNVLNHLND 1110
m-PC	1128 H	HTVPVEAASAALRRLSVCGRTLSLDLATSGASASEAQGRKKAAESRLGCGRNL 1180
T416	1111 G	GKHELMDASELVAEINKLLQDVRQS

FIG. 61

60 120 172	220	268	316	364	412	460	208
ω	24	40	56	72	& &	104	120
CAACTCTTTA CACTCGGCGA GCC TCC Ala Ser	GGT Gly	CTG Leu	CTC	TTT Phe	GCA Ala	GAC Asp	TAC
CAACTCTT CACTCGGC GCC TCC Ala Ser	GAA Glu	CCC Pro	CCC Pro	ACG Thr	GAG Glu	666 Gly	GAG Glu
•	ACC Thr	ACA Thr	CAA Gln	CTG Leu	CAA Gln	AGT Ser	GGA Gly
TCTCC CTGCT GCT G	ACG Thr	ATC Ile	TCC	AGT Ser	CAC His	AAG Lys	GCA Ala
GTGTCTCCGT CGCCTGCTCC AGG GCT GCC	CTG	CAG Gln	TAT Tyr	AAG Lys	GAT Asp	CTG	GAA Glu
~ ~	GCG Ala	ACT Thr	TTT Phe	TGG Trp	GGA Gly	AGG Arg	GAG Glu
AATCCCGGCT TCTACCGGGC G ACG TGG	TGG	666 Gly	ATC Ile	TTT Phe	TTT Phe	TGG	CIG
FH (1)	CTG	666 Gly	AAT Asn	TGG Trp	TTT Phe	CCA Pro	CAG Gln
(·) H	CIG	GCA Ala	TGC Cys	ACC Thr	GAA Glu	TCT	ATC
GCCGGCTGC GCCCTTGGC CCGCGGGCG	ATT Ile	ATG Met	TTC Phe	ATC	TTT Phe	GTG Val	GGA
	CTG	ATG	ATA Ile	GGT	GTC Val	ATT	CCT
AAAG CCCC AGCA	CTC	GAG	ACC	ATG Met	AAA Lys	GCC	CTG
GTGCAAAAGC GTCTCCCCCT ACAACAGCAG	GCG	GTA Val	GTC	TCT Ser	GTC	GGA Gly	CGG
	GCG Ala	AAA Lys	AAT Asn	ACG Thr	GAA Glu	CCT Pro	CIG
GAAGTGGGAT CGCAACAGAG AAAAATTAC	TGC	CIG	GAC	ATC	AAA Lys	CGA Arg	TCA
GAAGTGGGAT CGCAACAGAG AAAAATTAC	ACG Thr	GAT Asp	AAT Asn	AAC	GAC Asp	TTC Phe	GCC Ala

Fig. 7A

COVECIEC STREET

556	604	652	700	748	796	844	892	940
136	152	168	184	200	216	232	248	264
CAG	GTG Val	TTC Phe	TTT Phe	ATC Ile	AAC Asn	CAT His	GCT Ala	CAT
GTC	CAA	666	AAG	ACC	CTG	CGG	GCT	ATT
Val	Gln	Gly	Lys	Thr		Arg	Ala	Ile
ACA	GAT	AGT	CAG	CCC	AAG	GTA	ACT	TCC
Thr	Asp	Ser	Gln	Pro	Lys	Val	Thr	
GGA Gly	CTG	TCA Ser	ACC Thr	GGT	TIG	GTG Val	CTG	TTT Phe
CAG	TTG	GAG	CAG	ACT	TGC	TGT	ACC	AAT
Gln	Leu	Glu	Gln	Thr	Cys	Cys		Asn
GCA	TTG	TGT	AAG	ATC	AGC	CAG	TTT	GAT
Ala	Leu	Cys	Lys	Ile	Ser	Gln	Phe	Asp
AAG	AGA	ATG	GAG	GTC	ACT	TAC	AAC	ACA
Lys	Arg	Met	Glu	Val	Thr	Tyr	Asn	Thr
CTG	AGC	TAT	TGG	GAT	GTC	GTC	AGC	AAG
	Ser	Tyr	Trp	Asp	Val	Val	Ser	Lys
CCT	GCC	AAA	ACA	GAG	AAT	ACT	AGG	GAG
	Ala	Lys	Thr	Glu	Asn	Thr	Arg	Glu
ACC Thr	CCA Pro	GAC Asp	ATA Ile	TCT	TTT Phe	666 Gly	TTG	ACT
GTC Val	TCC	GAA Glu	AAT Asn	ATT Ile	ACA Thr	CCT	CCC Pro	GAA Glu
GTG	GCT	AAT	ATT	GAG	66C	GAC	ACC	TCT
Val	Ala	Asn	Ile	Glu	61y	Asp	Thr	Ser
GTG	GTG	GAG	GCT	ATA	GAT	GAA	CAT	CTT
Val	Val	Glu	Ala	Ile	Asp	Glu	His	Leu
GAG	GTT	AAA	GAG	CCC	ATG	CAG	TTG	AGT
Glu	Val	Lys	Glu	Pro	Met	Gln		Ser
TGT Cys	GAA Glu	ATG Met	CCA Pro	CAT His	AAT Asn	TCT	TCC	CAC His
CGA	CTT	GGC	TAC	CCC	AAG	TCC	GCG	CGG
Arg	Leu	Gly	Tyr	Pro	Lys		Ala	Arg

Fig. 7C

odymaise ostania

GCCCAAATAG	GCCCAAATAG TAAATAAAAC AGCTCAAGCT TTAGAGGCCC AAGAGACCTA TGTAAATGTG	AGCTCAAGCT	TTAGAGGCCC	AAGAGACCTA	TGTAAATGTG	158
TTGGTTAAAA	TIGGITAAAA TAGITITAGA TAATAAAAGG GCCCICAAIT	TAATAAAAGG	GCCCTCAATT	ATTTATGGGC CTGTCAAGGC	CTGTCAAGGC	16
AAAATCTGCA	AAAATCTGCA CAACAGCCAG	TACATCTCAT TATAAATAAT	TATAAATAAT	TTAGGAGAAG TGGAATAATC	TGGAATAATC	17(
AGTCAATTAA	AGTCAATTAA GAAAAATGGC	CCTTTATCTA AAGTTGGCCA	AAGTTGGCCA	TITAGATICA CGGGACTIAI	CGGGACTTAT	17(
TCCTGTTGGA	TCCTGTTGGA TCTAGGCCAT	GAGAAAACTG	GAGAAAACTG GATAAAAAGT	GGTTTTCAAA TGTTTCTTGT	TGTTTCTTGT	182
GGTATTTGTG	GGTATTTGTG ACTGTTGTCA		TATTICITGC CITICICIGG	TTCTGATATT CAGGIGCTAT	CAGGTGCTAT	188
TGAGAGAGGA	TGAGAGGA GGAAGGAAGA AACTAGTCAG GCAGGCAGTT	AACTAGTCAG	GCAGGCAGTT	AGGGTGGGCC CTCAGTCAAA	CTCAGTCAAA	194
TICCTICAAA	TICCTICAAA CAAAAGAACA GCCIGAAAAA ICAAACIGCA GAIAAGGGAA	GCCTGAAAAA	TCAAACTGCA	GATAAGGGAA	CTTGTACAGG	20(
CGGGCTTGCC	GGGGCTTGCC TAAAACATGC		ATACATTAAA	CCACAGCCAC ATACATTAAA ACAAGGCTAC ACAGGAGACT	ACAGGAGACT	20(
TGCCTAGACA	TGCCTAGACA TGCTCACAAT		ATCCCCTGAC	AGAAAATTCC ATCCCCTGAC ACATGCACAG TAAGGGGAAC	TAAGGGGAAC	212
AAAGCCACAT	AAAGCCACAT GGAGTAACTC	AAGCTAAGGG	CTTGCATGCA	CTTGCATGCA CACTACGAGG ATGGGGTGGA	ATGGGGTGGA	218
GCTACCAGAA	GCTACCAGAA ATGTGTGCCT	TATGCCTTTG	TATTCAGCTG	TGAAATGGCA ACCCTCTTTT	ACCCTCTTTT	224
CECCCCCTC	GGGCCCCTC TCTGCAGTGG	AGTGCTTTCT	TCTTTTGCTT	ATTAAACTTT CACTTCAACT	CACTTCAACT	23(
TCAAAAAAA	тсарарара дарарарара дарарар	AAAAAA				23,

Fig. 7D

<u> corealso citasos</u>

2246	2186	121196	2126	121256	2066	121316	2006	121376	1946	121436
GAGAGGGGGC GAGAGGGGGC	ATTTCTGGTA	ATTTCTGGTA	CCATGTGGCT	CCATGTGGCT	CATGTCTAGG	CATGTCTAGG	TAGGCAAGCC	TAGGCAAGCC	TGTTTGAAGG	TGTTTGAAGG
CTCCACTGCA	TAAGGCACAC	TAAGGCACAC	TTGAGTTACT	TTGAGTTACT	CTATTGTGAG	CTATTGTGAG	GGGCATGTTT	GGGCATGTTT	GCTGTTCTTT	GCTGTTCTTT
GAAGAAAGCA	TACAAAGGCA	TACAAAGGCA	AGCCCTTAGC	AGCCCTTAGC	ATGGAATTTT	ATGGAATTTT	ATGTGGCTGT	ATGTGGCTGT	GATTTTCAG	GATTTTTCAG
ATAAGCAAAA 	CACAGCTGAA	CACAGCTGAA	TGTGCATGCA		GTGTCAGGGG	GTGTCAGGGG	GTTTTAATGT	GTTTTAATGT	TCTGCAGTTT	
TGAAAGTTTA		GITGCCATT	: ATCCTCGTAG	ATCCTCGTAG	_	TACTGTGCAT	_	GIGIAGCCII	AGTICCCTIA	AGTICCCITA
GAAGTTGAAG	CCAAAAGAGG	CCAAAAGAGG	GCTCCACCCC	GCTCCACCC	TIGITCCCCT	TIGITCCCCT	CAAGTCTCCT	CAAGTCTCCT	CCCCTGTACA	CCCCTGTACA

Fig. 9A

1886	161490	0 7 0 1	121556	1766	121616	1706	121676	1646	121736	1586	121796
			CAATAGCACC TGAATATCAG AACCAGAGAA AGGCAAGAAA TATGACAACA GTCACAAATA 12	CATTIGAAAA CCACTTTTTA TCCAGTTTTC TCATGGCCTA GATCCAACAG	ccacaagaaa catitgaaaa ccacititia iccagititic icaiggccia gaiccaacag 12	CGTGAATCTA AATGGCCAAC TTTAGATAAA GGGCCATTTT TCTTAATTGA	GAATAAGTCC CGTGAATCTA AATGGCCAAC TTTAGATAAA GGGCCATTTT TCTTAATTGA 12	ICCT AAATTATTTA TAATGAGATG TACTGGCTGT TGTGCAGATT	CIGATIAIIC CACTICICCI AAATTAITIA TAAIGAGAIG TACIGGCIGI IGIGCAGAIT 12	. ATAATTGAGG GCCCTTTTAT TATCTAAAAC	TIGCCITGAC AGGCCCATAA ATAATIGAGG GCCCTTTTAT TATCTAAAAC TATTTTAACC 12
•											

Fig. 9B

1526	1466	1406	1346	122036	1286	122096	1226	122156
AAAGCTTGAG CTGTTTTATT TACTATTTGG 	CATGITITAG TITAGAAATA CCTAGIGAGG 	CTGGTGGTCA GTTATTGATC AGATAAAATA	GAGAAAACA	CTAAATGTGT GAGAAAAACA AGCAGTCCAC	AGTCTGGTTC ATTCACAGAG ATATAATACT	ATTCACAGAG	TACAACACAT CACCCCAGAG TCACAAACCA	CACCCAGAG
AACACATTTA CATAGGTCTC TTGGGCCTCT AN IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GCCATAGTCA GGGATAAAAA TGTTTAGAAA CAAAA CAAAAA TGTTTAGAAA CAAAAAAAAAA	GTTAGAAATT CTTAGTCAAA CTAGTGAGAT C' 	CCCTCTCTAA GCCATAGTTT	TGAGGAATIC CCCTCTCTAA GCCATAGITI C	ACATAGTTCA GGGCCTGGTC TGAACACTAA A	GGGCCTGGTC TGAACACTAA	TGTTTAGTAT GGAGAAAGAG AGGGAGGCTT T	GGAGAAAGAG AGGGAGGCTT

Fig. 9C

1166	1106	1046	986	926	904
ACTGGATTGG ACTGGATTGG	CCTTTCCAGC CCTTTCCAGC	TTTTACTAGC TTTTACTAGC	GAATCAAAAC GAATCAAAAC	TGGAAAATT TGGAAAATT	
GTGATAGGAA GTGATAGGAA	CTGACAAAGT 	TCTAAAAGCT TCTAAAAGCT	TTTTCCAAG TTTTCCAAG	CACCAATGAA CACCAATGAA	
TAGGTCCTCT TAGGTCCTCT	TGAAGAGGGA TGAAGAGGGA	CAGCAGCTGC	GCCCCTTACC 	TGAAATAGGC TGAAATAGGC	
ATGTGACAGC	CACCTGATGG	GTAAGGTTGG GTAAGGTTGG	TTGCTTTGGA TTGCTTTGGA	CACCAATGAA 	AA CA
GTCAGATGGT 	AACACAGCCA ACATTCCCAA	AGGCCTGTCC CTTGAGGCTT	CCAAGACACA GGGCTGAACT 	AATTAATAAA ACCAGTCCAA 	ATCTGTCTTC TCAGTTTCAG AA
CCATACAGAG	AACACAGCCA	AGGCCTGTCC 	CCAAGACACA CCAAGACACA	AATTAATAAA AATTAATAAA	ATCTGTCTTC

Fig. 9D

2	22 137	42	62 257	82 317	102 377	122 437	142 497
V GTG	$_{ m ITG}$	G GGA	Y TAC	L CTG	TACC	$_{ m L}$	GGT
M ATG	A GCT	C TGT	T ACC	I ATT	${ m F}$	L CTC	R CGG
GTC	L CTG	9 66C	G GGG	L CTG	L	E GAA	9 9
3000	L	D GAT	P	R AGA	L CTT	K AAA	s TCT
CCAAGCTGGCGCCCAGCGGGGTC	9 9	G GGT	Y TAT	K AAA	$^{ m Y}$	P	I ATT
99099	R CGG	L	N AAT	999	D GAC	V GTT	H CAC
AGCTO	GGG	E GAG	K AAG	K AAG	S TCT	T ACT	s TCC
SCCA.	A GCC	E GAG	S TCT	P CCA	A GCT	M ATG	G GGA
SCTTO	A GCT	A GCG	T ACA	V GTA	C TGT	S AGT	S AGT
CGAC	R CGG	Q CAG	M ATG	T ACA	T ACC	G GGA	E GAG
GGGGAGGC	A GCG	L CTG	T ACA	I ATT	Q CAG	C TGT	F TTT
4GGG	L	R CGG	9 88C	T ACA	S TCC	Y TAC	R CGC
3TCG2	A GCA	L	S AGT	K AAG	E GAA	P CCA	V GTC
ATCC	9 990	P CCG	D GAT	E GAA	I ATC	G GGT	T ACC
26667	9 9	A GCC	Q CAG	C TGC	D GAT	Y TAT	V GTA
3GCT(299 9	S TCC	Y TAT	V GTT	$_{ m L}$	Q CAA	E GAA
TGC	R CGC	V GTC	T ACT	T ACT	D GAT	D GAT	S AGT
3CAG(A GCC	A GCG	V GTG	H CAC	G GGA	S TCA	T ACA
GGCCCGGGCAGCTGCGGCTCGGGATC	9 9	L CTC	L CTA	N AAT	L TTG	S TCT	N AAC
)))99	P	L	H CAC	P CCC	R AGG	S AGC	Γ

Fig. 10A

162 557	182 617	202	222 737	242	262 857	282 917	302 977
A	A	A	R	S	E	Q	9
GCT	GCA	GCT	CGC	TCC	GAA	CAA	9
R	V	K	Q	GGT	F	D	S
CGA	GTA	AAA	CAG		TTT	GAC	TCG
E	D	C	L	D	S	G	A
GAA	GAC	TGC		GAT	AGT	GGA	GCT
L TTG	R AGA	Γ	V GTG	R AGG	$_{ m ITG}$	S AGT	W TGG
C	C	L	S	S	S	E	S
TGT	TGT	TTA	AGT	TCG	TCC	GAG	TCA
T	G	S	I	L	R	N	P
ACA	GGT	TCT	ATC		AGA	AAT	CCA
I	A	TACC	Q	V	S	V	ე
ATA	GCT		CAG	GTT	AGC	GTC	ე
L TTA	P CCA	, D GAT	9 9	GGT	C TGC	S TCG	Q CAA
D GAT	C TGC	R AGA	GGT	N AAT	G	Q CAG	D GAC
P	F	Y	L	A	N	W	Q
CCA		TAT	CTA	GCC	AAT	TGG	CAG
H	K	G	E	L	S	S	L
CAT	AAA	GGA	GAA	CTG	TCC	TCA	
D	S	D	D	I	T	S	R
GAC	AGC	GAT	GAT	ATT	ACC		CGA
S	Y	V	A	999	F	S	A
AGC	TAC	GTA	GCT		TTT	TCT	GCC
S	E	M	I	E	L	A	Q
AGC	GAA	ATG	ATT	GAA	CTG	GCT	CAA
A	T	N	I	Y	F	R	ე <u>ე</u> ნ
GCG	ACA	AAT	ATA	TAT	TTT	AGA	
Y TAT	K AAG	999	G GGA	R CGA	R CGA	I ATC	P
T	$_{ m L}$	S	A	S	K	Q	S
ACC		TCT	GCA	AGT	AAG	CAA	TCT
L	Y	I	H	I	D	999	W
CTG	TAT	ATT	CAT	ATC	GAC		TGG
$_{ m L}$	H CAT	D GAC	I ATC	999	S TCA	D GAC	H CAC
F	S	G	A	K	L	PCCT	V
TTT	AGC	GGA	GCC	AAA	CTG		GTT

Fig. 10B

382 1217 402 1277 422 1337 442 1397 342 1097 362 1157 K AAG K AAG V GTG N AAT R AGG V GTG T ACA I ATT N AAC Q CAG I ATC L ITG I ATT GAG Y TAT GGA Q CAA H CAC T ACA S TCA A GCT G GGG F TTT K AAA V GTG $\overline{\mathbf{W}}$ D GAT E GAG V GTG Y TAT PCCA T ACA T ACG N AAC N AAT D GAT F TACC D GAC Q CAG GGT E GAA T ACA N AAC K AAG R CGG P Q CAA K AAA I ATT E GAG S TCG W TGG F TTT V GTC TACA K AAG N AAC I ATA I ATT TACT Q CAG K AAG N AAC V GTT W TGG Q CAG G GGA S TCT S TCT R s TCA TACA E GAG N AAC V GTG T ACA N AAT C VGTT s TCT N AAT GGT $\mathbf{Y} \\ \mathbf{TAT}$ CGA GGA GGT S AGT S TCC N AAC Q CAG T ACC T ACA R AGA I ATT T ACA PCCA A GCC E GAA TACC K AAA F TTT L S AGC H R AGG FITC V GTG V GTG E GAG Q CAA EGAA K AAG I ATC s ICG I ATT N AAC V GTG S AGT M ATG N AAC PCCC K AAG T ACA PCCC GGA E GAA E GAA $_{
m L}$ K AAG I ATC V GTG PCCT I ATC R CGC P N AAT A GCC I ATA W TGG FTTC N AAT S AGT

Fig. 10C

542 1697 502 577 562 1757 582 1817 602 1877 622 522 1637 K AAG K AAG N AAT Q CAG D GAC Q CAG T ACG R R AGA W TGG D GAT Q CAG M ATG P A 3CC Y TAC Y TAC $^{\rm C}$ $_{\rm TAT}^{\rm Y}$ P Y IAC F TTT C TGC 9 9 A GCC D GAC S AGC D GAT R D GAC E GAG S AGC I ATC A GCA TACA A GCA FY TAT P Q CAG FTTT K AAA TACC M ATG T ACC H CAC E GAG A GCG IATC Q CAG FTTT D GAT S ICC G G G G P S ICT GGG A GCT E GAG S AGT G GGC GGC P FTTC T ACG M ATG E GAG A GCT T ACA K AAG A GCC A GCG I ATC $_{
m L}$ H CAC GGA A GCA S TCA R AGG D GAT A GCT Q CAG L TACG TACC PCCC A GCC S TCA V GTC S AGC R GGC F TTT GGA H CAT D GAT L V GTG Y TAT R AGA L TTA T ACA V GTG A GCG Γ L K AAG GGG G GGG Y TAC V 3TG P A GCC V GTC S AGT F TTT Q CAA T ACC A GCA E GAG H 9 66C E GAG R CGG P T ACA H CAC V GTT GGA L K AAA Y TAT M ATG I ATT E GAG R CGC E GAG V GTG K AAG E GAG M ATG A GCC GGC K AAA V GTG K AAG A GCC I ATC K AAG I ATT LCTC D GAT Q CAG E GAG P ${\mathbb T}$ R P L ITG K AAG

Fig. 10D

642	662	682	702	715
1997	2057	2117	2177	
V	D	D	C	
GTA	GAC	GAC	TGC	
PCCC	A GCG	PCCT	D GAC	
S TCC	PCCT	H CAC	R AGA	
F	Q CAG	G GGA	P	
9	A	S	A	
9	GCA	AGC	GCC	
ე <u>ე</u> ნ	S AGC	E GAA	S TCT	
S	H	T	Y	*
TCG	CAC	ACC	TAT	TGA
S	P	A	S	$_{ m ITG}$
TCC	CCA	GCC	AGC	
L	R AGG	L	D GAC	L
S	Q	A	S	A
	CAA	GCC	AGT	GCC
H	Y	S	T	TACT
CAC	TAT	AGC	ACG	
K	D	V		M
AAA	GAC	GTC	GGG	ATG
H	G	A	CCC	A
CAC	GGA	GCT		GCC
9	D	K	H	T
66C	GAC	AAA	CAT	ACG
P	Q CAG	PCCC	T ACG	Q CAG
Q	A	R	P	N
CAG	GCC	CGG	CCA	AAC
P	9 9	D GAC	CCC	L
999	V GTG	Y TAC	K AAG	P
P	GGT	9	Q	T
CCA		9	CAG	ACA
V	A	R	S	L
GTC	GCG	AGG	TCT	

2377 2456 2535 2614 2693 IGAAAATTTTTAGATGGCGTTTTCATTCCTCTGACTGATATTGAGCTGCTTTGGTGTTAAAGGTGTAATGTGTACAGAG CAGCTGTTGCAAAATGTATAAATAGTATGTTCATTTTTTCAGTATATTATCTGATACTGTTAGCAGCAGGTCTG ATACTGTTTACAAAATTGTGCAGCTGGTTTCGTGCTGACCCTTAGGGTGCGTCTGTTGGGTTTTGTTGGGCTAGAAAA TTGTATTTAACAATAATAAAAGTAACTTAAGTTTGCTCTATCAGATTTTTAGTTCTGCACAGAGGTTAAGTGGGAAAATG

Fig. 10E

COZECLEC CELECT

7	CHATCCAAACCAAATAAAAAAAAAAAAAAAAAAAAAAAA
35	AGCTGCTGGTTAGTGTGGAGGGGAAGTGGTTTACTTTGTAGAGTTTTACATGGTTTTATGCGCACACTAATTGTAATAAA 35
34	CCCTATTTGTGTGTGTTATTACATCCTGTGAAATGTATATATGTTAAAATAATGGGGGGGG
34	TGCCAAAGAGGGAAGTGTGTGTTTTTTTAATAGAAAATATGGACCAAAAATTTTTTTCCCTGAAGAATGTATTATAA 34
33	GACATCAGCTGTACCTCATGCTCAGTAGTTTTTATTTGAGTTTCTTTTGTGAGTTAACTATGGGAGATTTAACCTCTTT 33
32	GAAACTGTTGGAAACTGATCTCATTTTATAAGAAATGATTTTCCCCTCAAGGAGGCGTCTGTAATTCCAGAACAGTCCA
31	CTGAAAAACAAAGTTATTTGGAACATGTTCATGCAAAAGTGATTCTGACCAAGTCTAAATCGAGCTTTTCTACTGACAT 31
30	AAAATATTGCTGAGGTCAGACGCCACAATTTTCATGACTTTCTTCAGAAGTAGCACATTTTCGTGACTTCCGCTGTCCT
30	CCCAGCTCCGGTGACCATGAAGGTGGCACAGGAATTACAGTGTGAATGGCTGTGTCAGATGTTTTCGTACCTCAGATTA 30
29	AAAACAAGCAAAGAAACAACCACCTCAGCAGCTGCCCGTTTCCTTAGTCTCCACTTCAGAGGGGGATGCGAAGAGGTCGG 29

Fig. 10F

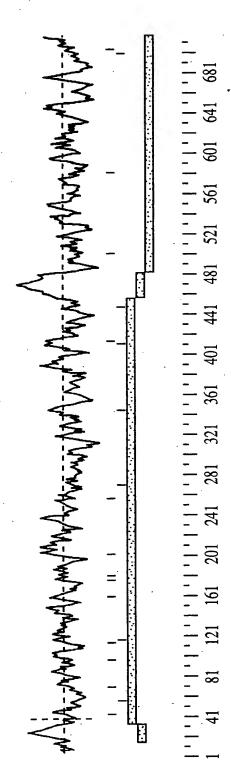


FIG. 106

65/361 65/361 79 158 340 14 220 34 280 54 460 94 114 520 134 580 GTGGTCGCGCCGAGGTGAGACTGTGAAGAAGAACGTTGCTTGGGCAAAAAGGAGCATATTCTCAGGAGACGGGGC GAC GAA AAA AGT AGT CAT വ Ω ¥ 田 വ 団 GTG AGC AAA AAA \gt AAT GAG TAC ¥ ഗ ¥ × 回 Z GTA AAC CCC 999 IGG CCA ATT വ z Ŋ ⋈ Д Н GTG TGC TTA \gt TTT ICI ACG TTT C Ы ഥ ß ഥ ₽ ATT ATT ATT GIC TCA AAC GGC > Н Н വ r Z CTT Q CAG CAG ACA Ы GIC ATT GAA Ø Н 闰 Н > 999 ტ TCA GGA CCA ICT ATT LLL Д Ö വ ഗ ഥ Н $_{\rm TCT}$ വ GIC TAT TAT TIC TACT GCA > Ø × × ഥ ATC AGC TAT ACA ICC TIG AAG \succ വ ഗ \vdash × П ATC GAG LCIT GGA AGG L TTA ACA O ഷ ⊣ 臼 ATG Σ ACA ICC GCT LCTA TAT ITC \succ Ø H ഥ വ CAC ACC AGC 田 LLI TTT GAT GGA ഗ Ŋ Ω ᅜ Н ഥ TGG ⋈ AGG ATT ACT L TTA TGT AAA Ö × α HН AAC TIC TACC ACC ATA z GGA AGA r Н ഷ \mathbf{H} ഥ ATG Σ ATG ACC GGC GCA GAC AAA ď Ω Σ \vdash Ö × GCCCCTGCAGCTCCTTCATC ACC CAG AAC TGC GGA CAA CAA Ö Ø Ö Н Z GTT TIC CCC IAT TTT CTT П > Œ, Д \succ ഥ GAC GIT AGT GGT TTITTT> Ö വ ഥ Ω 됴 GAT AAG AAA CCA GAA AGG 团 ഷ × X О Д AAC ICC AGC CIG CTT IGG П L ഗ ⋈ Z ഗ

Fig. 11A

oover of the contract of the c

									6.	3/36												
154	640	174	700	188	745	824	903	982	1061	1140	1219	1298	1377	1456	1535	1614	1693	1772	1851	1930	2009	2088
Z	AAT	യ	TCA			LTAC	BATG	STAC	ACTA	FICC	TCT	TLL	BAGC	IGAA	AGTA	TLC	CTA	CAC	BAAG	IGCT	ATAA	TOL
₽	ACC	` &	GCA			[CTT]	\CTG(rgTA(CAT	ATAGO	3AGG(ATTC	AAGGC	rttcj	LTTG	ATCC	rgal	TAAG	CTG	\CTC1	TGL	ATGAC
>	GTT	Ø	GCT			[GAT.	3GGG7	TITC	rata(AAAC?	AGCAC	3CAG(AGCC2	ATA	\GGT.	\TTC?	PACA	GGAZ	CACZ	TAT	3ACC?	AGTA2
Z	TTC AAT GGC AAT GTT ACC AAT	Д	GAT			GCAACTCTTTTGAATCCATACAGGTCGTCTGGCCAATGATTCTTTTAC	GCCCATTTGGGAAACTGAGCTTCTTTCTTCTGCACTGGGGGACTGGATG	TACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTAC	GTCTGTTGACAGGGTTTGTTTTTTTTAGCCTCAGAGTATACCATACTA	AAACATTATTAGGGATTACCATGGTGGAAGAGGGATAAACATAGGTCC	CCATTCACATGCCCCTCCTAACTCCACAAGCGAGGGTAGCAGAGGCTCT	GAGGGCTCCTAGTGCTGAGCTTGGAGCAGCACGGACAGCAGCATTGTTT	GGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAGGGAGC	AGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAA	AACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTTGAGTA	TTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTCATCCCTTC	GCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA	AGAGAAGGGCTGCTCAGGGAAACATTGGCTGGGGGCACGGAATAAGCAC	GAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAG	AGTACCCTGGCTGTTCTCCACACTCACAGACATCAGCTATACTCTGCT	'TTTGTGTTTTGAGTAAGAATAATTAAACCATAAGGAAGACCATGTATAA	AGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT
ტ	GGC	ഥ	m TTT			CTGG	CTGC	3AGG	CCIC	AGAG	3CGA(CACG	4ACC	rccc	IGCT(CACA	4TTG	rggg	rcat.	3ACA	ATAA(rgtA(
Z	AAT	Н	ACA	*	TGA	rcgT(l'CTT(4GAT(rtag(rgga i	4CAA(3CAG(4GAA	AAAT	CCTT	L'AAT	4CTG	rggC	BAGT	4CAA(AACC/	4CAA
ഥ	TTC	×	AAG	×	C TGT GAG AAG AAT GCC AAA TGA	CAGG	ICTT.	ATAG	ratt.	ATGG	CICC	rggA(rtgai	CTAA	3CTT(ACAA.	rggC2	ACAT	CAGG(ACTC2	ATTA	AATA
>	AAC TCT GTG 1	₽	ACA	Ø	GCC	CATA(AGCT.	ragT?	3TTT.	racc2	CTAA(AGCT.	CCCT	raag(3CAG(3GCA/	₹GCC.	3GAA	3AAA(CCAC	AATAA	STCT
യ	TCT	П	CTA	z	AAT	AATC(ACTG	CAGT	3TTT(3GAT	CCIC	3CTG	AGAC	CACT	3TAA(CTTA(AAGG.	ICAG	ACAG(LTCT(L'AAG	lTGT(
z	AAC	ט	ggc	×	AAG	rttg.	3GAA	AACT(CAGG(LTAG(rgcc	ragT(rrgg.	3AGA(LTAG(3TCT(מממי	CIGC	rgag;	3CTG	rgag'	CATT
Z	AAC	Н	ATT	闰	GAG	ICTT	LTTG(AAAC	rTGA(LTAT.	CACA	CICC	CTTC	IGAA(AAAT	3ATA(CTGA(₽GGG(CACC	CCTG(3TTT.	ATAC
Н	ATC	₽	ACC	บ	IGI	CAAC	CCCA	ACGG7	ICTG	AACA:	CATT	AGGG(3AAC(3000	ACCA	rttg(CCTA(3AGA	AAAT(3TAC(l'TGT(3CAC
Z	TGG	Ą	BOB	Н	ATC		CTTG		CTAG	LATA	ACCC(3GGG	ATAG	CAAA(ACAG(AAAA(ATGG.	rggA(CCLL	
ഷ	CGT	ט	$_{ m TGT}$	ద	AGG	rata(3GTC(rcag	AGGC(AAAT	3GGA	CCLIC	CAGG	rcag(CCLL	LTTA	AGGC.	ragg;	ICAA	3TCT.	3ATG(AAAG
Z	TGG	Z	AAC	ద	CGC	BAAC	PAGC	4GGA	AAAAJ	rgagi	rcaa(l'TGG(rggg(LTCL	AACT(L'ATT.	racc;	AGAG	4GGG	4CAA(4AGA(CACC
ద	AGG	ᅜ	$_{ m LLC}$	X	TAC	ACAA(CCAG	AGAC.	3ATC	AGAG	BITC	AGGC	BGTC	rcrg	ATGT/	IGAG	CTGA	CCGA	CATC	3AAG	AGAA	ragT(
×	AAA	Z	AAT	Ø	AGC	rgtg;	rcta(CAGG	3ACT(CTGT/	CTCT(ACTA	3AGA(BATT	ACAT.	LTGT	AAGC (3000	3GAA(AGAG	AAAG.	ATAA
田	GAG	Ø	CAG	Н	ATC	rccc	ICTG'	ICTC	ITCT(3TAA	rcgT(CTGA	TGGA(ACTA(TATA	GTAT.	GAGA	ICCA	AAAG(AGAA	TAAG,	3GAA.
田	GT GAA GAG AAA AGG TGG CGT TGG ATC AAC	Z	AG AAT CAG AAT TTC AAC TGT GCG ACC ATT GGC CTA ACA AAG ACA TTT GAT GCT GCA TCA	Д	GT GAC ATC AGC TAC CGC AGG AT	CACAGTTCCCTGTGACAAGAACTATACTT	TACCTATCTGTCTACCAGTAGCGGTCCTT	TAGCCATCTCCAGGAGACAGGATCAGTTT	GAGCATTTCTGACTGATCAAAAAGGCCTA	TAGGGAGTAACTGTAGAGTGAGAAATTAT	GTGACTTCGTCTGTTCTCAAGGGAACC	CTCAGTCTGAACTAAGGCTTGGCCTTGGG	TGGGAATGGAGAGGTCTGGGCAGGATA	AAACACACTAGATTTCTGTTCTTCAGCAA	CTCCATTATAACATATGTAACTCCTTTGT	CTGGCTGTATTTGTTGAGTATTTTTAAAA	GTTCTGGAGAAAGCCTGATACCAGGCACA	AACTGGTCCAGCCGCCGAAGAGTAGGAAA	TAGTAAAAAGGGAACATCAGGGTCAAATG	AAGGCAAGAAAGAGGAAGACAAGTCTTGG	'GGTGCATAAGAAAGAGAAAAGAGATGCCT	ACTGATGGAAATAATAGTCACCAAAGTAC
ద	GT	Ø	'AG	ט	ĞŢ	ĊĀ	'TA(TA('GA(TA(GT(CT(ŢĞ	AA	CT	ij	GT.	AA(TA(AA(GG.	AC.

Fig. 11C

AAAAAAAGAA 4074

14 220	34	54 340	74	94 460	114 520	134 580
2	2	m	. 4	4	5	5.0
r b	S	S	D	E	K.	H
	AGT	AGT	GAC	GAA	AAA	CAT
, V	K	S	K	N	E	Y
	AAA	AGC	AAA	AAT	GAG	TAC
V	N	9	P	W	P	I
GTA	AAC	999		TGG	CCA	ATT
V	F	F	C	S	T	L
GTG	TTT	TTT	TGC	TCT	ACG	TTA
I	I	I	V	S	N	, 299
ATT	ATT	ATT	GTC	TCA	AAC	9
CTT	Q	Q	T	E	V	I
	CAG	CAG	ACA (GAA '	GTC	ATT (
G	P	S	G	S	I	F
GGG	CCA (TCA (GGA 1	TCT (ATT (TTT 1
S	F	V	Y	T	A	Y
TCT	TTC (GTC	TAT (ACT	GCA 1	TAT
IATC	Y	T	S	S	L	K
	TAT	ACA (AGC 7	TCC 7	TTG (AAG
I ATC	CTT	GGA .	R AGG	L TTA	T ACA	E GAG
M	L	Y	T	F	S	A
ATG	CTA (TAT (ACA		TCC 7	GCT (
H	F	S	T	F	G	D
CAC	TTT	AGC '	ACC		GGA	GAT (
W	L	R	I	C	K	T
	TTA '	AGG	ATT	TGT	AAA	ACT (
N AAC	ACC	T ACC /	F TTC /	R AGA	GGA i	I ATA
M	M	T	. 299	A	K	D
ATG	ATG 7	ACC 1	9	GCA 1	AAA (GAC 1
CATC	G	T	N	Q	C	Q
	GGA 1	ACC A	AAC (CAA (TGC 1	CAG (
CCTT	V	F	P	Y	F	L
	GTT (TTC 2	CCC 1	TAT (TTT :	CTT (
AGCT	V GTT (GGT .	S AGT (FTT	D GAC	F TTT (
GCCCCTGCAGCTCCTTCATC	K	D	P	E	R	K
	AAA (GAT (CCA 7	GAA	AGG (AAG
))))	L	N	S	W	S	L
	CTT	AAC (TCC (TGG (AGC	CTG

Fig. 11D

ĸ	压	压	×	~	M	~	M	Н	Z	Z	ഗ	>	ഥ	Z	ტ	\bowtie	×	>	Z	154
CGT	GAA	GAG	AAA	CGT GAA GAG AAA AGG TGG CGT TGG ATC AAC TCT GTG TTC AAT GGC AAG TAC GTG AAC	TGG	CGI	$^{ m TGG}$	ATC	AAC	AAC	ICI	GTG	TTC	AAT	299	AAG	TAC	GTG	AAC	640
Σ	Д	Ø	ഥ	വ	ტ	Ω	П	ტ	Н	ц	Ø	×	⊟	×	പ	臼	Н	Ą	ტ	174
ATG	CCA	CAG	TTT	ATG CCA CAG TTT CCT GGG GAT CTT GGT TTG CTT CAA AAG ACC AAA CCT GAG ATT GCT GGG	999	GAT	CII	GGT	${ m TTG}$	CII	CAA	AAG	ACC	AAA	CCI	GAG	ATT	GCT	999	700
ĹΞι	T		ы	*																178
TIC	ACC	CTG	TIC ACC CIG GAA TAG	TAG																715
CTCE	AACG	CTG	ACACT	CTCAAACGCTGACACTTGACTCTGTT	TCTG	TTCI	GCTC	TTCT	CCTT	'TCTI	CCAA	\CCC.	ATCT?	ATTC(CTA	CTGCTCTTCTCCTTCCAACCCATCTATTCCCTATCTGTCTACCAGTAGC	CTAC	CCAGI	ragc	794
GGTC	CTTG	SCCC	ATTT(GGTCCTTGCCCATTTGGGAAACTGAG	AACTG	FAGCI	TCTI	TCTT	CTGC	ACTG	36666	BACTO	3GAT(3CTA(SCCA	CTTCTTTCTTCTGCACTGGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA	SAGG	AGACA	AGGA	873
TCAC	TTT	PACGG	3AAA(TCAGTTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGA	rcagi	TAGI	ATAG	'AGAT	GAGG	TCCG	CTTC	TGL	AGTAC	CTGA	3CAT5	LTCTC	SACTO	BATCA	AAAA	952
AGGC	CTAG	TCTG	3TTG2	AGGCCTAGTCTGTTGACAGGGTTTGT	3GTT1	GTTI	TAT	TTAG	CCTC	AGAG	FTATE	1CCA1	ract?	ACTA	3GGA(TITATITITAGCCTCAGAGIATACCATACTACTAGGGAGTAACTGTAGAGTGAG	TGT	AGAG 1	r GAG	1031
AAAT	TATE	AAACZ	1TTA	AAATTATAAACATTATTTAGGGATTA	3GGA1	TACC	ATGG	TGGA	AGAG	GGAT	PAAAC	CATAG	3GTC(TGT(3ACT!	CCATGGTGGAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAA	TCTG	STTCI	rcaa	1110
2999	NACCC	CATT	rcac?	GGGAACCCCATTCACATGCCCCTCCTAACTCCACAAGCGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGG	CCTC	CTAR	CTCC	ACAA	GCGA	GGGI	AGCZ	JGAGG	CTCI	CCT	ZAGT(TGAR	ACTAP	AGGCI	PTGG	1189
CCTJ)555°	3AGGG	3CTC(CCTTGGGGAGGGCTCCTAGTGCTGAGCTTGGAGCACCACGGACAGCAGTGCTTTATGGGAATGGAGAGGTCTGGG	IGCIC	AGCI	TGGA	GCAG	CACG	GACA	JGCAG	CAT	[GTT]	ratge	3GAA1	rgga 6	SAGAG	SGTCI	1666	1268
CAGG	ATAG	GAAC	CTT(CAGGATAGGAACCTTCTTGGAGACCC	SAGAC	CCCI	TTGA	AGAA	AACC	:AGGC	SAGCC	ZAAGG	3GAGC	CAA	1CAC?	CTTTGAAGAAAACCAGGCAGCCAAGGGAGCCAAACACACTAGATTTCTGTTCT	SATTI	rcrg	LTCT	1347
TCAC	CAAZ	JCCCC	CTGA	TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAAACTCCATTATAACATATGTAACT	ACACI	TAAG	CTAA	AAAT	JDDI.	TTGI	CAT	\TTT(TGAZ	AACTO	CAT	PATA	ACATA	ATGT?	AACT	1426
CCTJ	TGT	ACCF	AAAA!	CCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTTGAGTACCTGGCTGTATTTGTTGAGTATT	GTAR	IGCAG	GCTI	CCLT	'TGCT	CTGA	\AGG1	TLL	3AGT?	ACCTO	3GCT(STATI	TGTI	rgagi	LATT	1505
TTT	LAAA 1	TLL	3GAT?	TTTAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTCATCCCTTCAGTTCTGGAGAAAGCCTGATACC	CTTA	IGGCA	LACA	TAAT	CACA	ATAI	PATTC	ATCC	CTTC	CAGT	CTG	SAGAZ	AAGCC	TGAT	LACC	1584
AGGC	ACAG	SCCTA	ACTG?	AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTAGAACTGGTCCAGCCGCCGAAGAG	CAAGG	FAGCC	TGGC	ACTG:	ATTG	GCAT	CACE	TTGE	ATCT?	3GAAC	TGGI	rccae	3000	CGAZ	AGAG	1663

Fig. 11E

1742 1821

TAGGAAAAGAGAGGCTGCTCAGGGAAACATTGGCTGGGGGCACGGAATAAGCACATAGTAAAAAAGGGAACATCAGGG TCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAGAAAGGCAAGAAAGGGGAAGAAGACAA



GATGCCTTTTGTGTTTTGAGTAAGAATAATTAAACCATAAGGAAGACCATGTATAAAACTGATGGAAATAATAGTCACC	1979
AAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGTACATGTCATTGTATGTA	2058
ACAAGATTGTTGTAAATCATATTTTTTTTACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTGGCT	2137
CCTTAGCATGGCCACTTACAATTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTG	2216
AGTAATTTGTGTTTGAGATGGGGTGGAAATTGGAATTATT	2295
GGAAAGGATAAGTGCTACCGTTGAGAAGGAAGAAAGGCTGAGTCTAGGTGGAGAAAAAATATCAACAGAACTCTAGCCA	2374
AAGGCAAGCCCCAGAACTCAGACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAGAGAGAACTGTTGCTTCT	2453
ACTICCTATITCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA	2532
GTTTAATTTCCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGA	2611
GTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAATGT	2690
GATCTTTATTAGATAGCAGTGCCATGCTTTTAAAAAAAAA	2769
CACTITGITICIAATAIGCIGIGIGAAICAGIACAGITITCIIACCCITICIIGGICIIAAITICCTIACIGAIAAAAI	2848
GGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT	2927
TAGGAGAAGCATTTTGTGGAGGATTTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAAAT	3006
GTAGGCAAGCCACTTCATTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAATTTGTGCAAGTCAGAGAAG	3085
GGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGCCCAGCCTA	3164
GGTCAGCCAACCCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGGCCACCCTAGATCAGCTGA	3243
AACTCTAAGCACAAAAATAAAAAACTTATCACTGTAAAAAAAA	3322
CTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCTTTCGTGTATTGTTCATCCAGCAACCAGGATGA	3401
TCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAAAAAAAGCCATGAAATTNTAGCAAGCCACTGAATTT	3480
GAGTITICACTITGGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACT	3559
GATAAAATGGGGTWGTAATACCTATCTCAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA	3638
TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGSTAGA	3717

Fig. 11F

rae repaired and the

AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAATTTGTGCAAGT	3796
CAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGC	3875
CCAGCCTAGGTCAGCCCAACCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGGAGCCACCTAGA	3954
TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAA	4018

Fig. 11G

79 158	19 218	39 278	59 338	79 398	99 458
ACCA	G GGA	T ACC	C TGT	K AAA	T ACT
CCACZ	V GTT	F TTC	R AGA	G GGA	I ATA
CTGC	V GTT	GGT	A GCA	K AAA	D GAC
CTGC	K AAA	D GAT	Q CAA	C HGC	Q CAG
SGCC	L	N AAC	Y TAT	F TTT	L
CGGG	V GTG	S AGT	F TTT	D GAC	F TTT
GAGA	V GTA	K AAA	E GAA	R AGG	K AAG
TCAG	V GTG	N AAC	W TGG	S AGC	$_{ m L}$
ATTC	I ATT	F TTT	D GAC	E GAA	K AAA
GCAT	L	I ATT	K AAA	N AAT	E GAG
AGGA	999	Q CAG	P	W TGG	P CCA
CAAA	S TCT	P CCA	C TGC	S TCT	T ACG
TGGG	I ATC	F TTC	V GTC	S TCA	N AAC
TGCI	I ATC	Y TAT	T ACA	E GAA	V GTC
ACGI	M ATG	L	G GGA	S TCT	I ATT
AAGA GAAG	H CAC	L CTA	Y TAT	TACT	A GCA
SAAGG	W TGG	F TTT	S AGC	S TCC	$_{ m L}$
GAAG	N AAC	L TTA	R AGG	$_{ m L}$	T ACA
gagactgtgaagaaggaagaacgttgcttgggcaaaaggagcatattctcaggagagggggcccctgcctg	M ATC ATG	T ACC	TACC	F	S TCC
GAG? AGC?	ATC	M ATG	T ACC	F	G GGA

Fig. 11H

norsolen nettent

119 518	139 578	159 638	165 659	738 817 896 975 1054 1133 1212 1291 1370 1449 1528
W TGG	A GCG	R I S AGG ATC		FTAC SATG STAC STCT STTT SAGC FGAA CTTC
R CGT	C TGT	R AGG		CCTTT CCATAC CCATAC CATAC CATTC CATCC CTTCT TTCCT
W TGG	N AAC	R CGC		FGATT FGGGG TATAC TATAC TATAC AGCAC SATAT TATAT
R E E K R W CGT GAA GAG AAA AGG TGG	F TTC	Y TAC		CCAAT CCGC AGAGT AGAGT AGGCZ TTGTC TTGTC SCATC
K AAA	N AAT	S AGC		TIGGG TIGGG TIGGG TIGGGG TIGGGG TIGGGGGGGG
E GAG	Q CAG	I ATC		CCGTC CCTTC AGATC TGGAZ AGAAZ AGAAZ AAATTC CCTTC
E GAA	N AAT	D GAC		CAGGI TATTI TATTI TATTI TAGA TTGA TTGA TT
R CGT	Q CAG	C TGT		CATAC TAGETZ STTT STACCZ CTAAC CCCT CCCT SCCCT SCCAZ
H CAT	N AAT	S TCA		AATCC CAGTI STTTC SCTCC SCTCC CACTI STAAC
Y TAC	TACC	A GCA		TTTGA SGAAA AACTC CAGGC TTAGC TTGGA TTGGA SAGAC
I ATT	V GTT	A GCT		ICTITICATE TARACT TERMINE TERM
L TTA	N AAT	D GAT		CAACT CCCAT CCCAT CATTC CATTC CATTC CATTC CCCAACC CCCAACCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCAACCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCAACCCAACCCAACCCAACCCAACCCAACCCAACCAACCCAACCCAACCCAACCCAACCCAACCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCAACCCAACCCAACCCAACCCAACCCAACCCAACCAACCCAACCCAACCCAACAACAAC
3 3 3 3	ე ტ	F TTT		CTTGC CTTGC CTTGC CTAGC CTAGC CAAAC CAAAC CAAAC
I ATT	N AAT	T ACA	* TGA	TATA(SGTCG SGTCG SGGA SGGAZ SGGAZ CCTTC CCTCC CCTTC C
F TTT	F	K AAG	K AAA	SAAC TAGC(AGGA/ AAAAA TGGG(TTCT/ TATT/ TACC/
Y TAT	V GTG	T ACA	A GCC	ACAAC CCAG SATCA SATCA STTCT SGTCT CTGT CTGT
K AAG	S TCT	L CTA	N AAT	rgrgi caggi caggi cagri cagai sagai ragai
D A E K Y F I G L I Y H GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT	I N N S V F N G N V T N Q N Q N F N ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC AAT CAG AAT CAG AAT TTC AAC	ე <u>ე</u> ნე	C E K N A K * TGT GAG AAG AAT GCC AAA TGA	TCACAGTTCCCTGTGACAAGAACTATACTTGCAACTCTTTTTGAATCCATACAGGTCGTCTGGCCAATGATTTTTTACCTATCCTATCTTTCTT
A GCT	N AAC	I ATT	E GAG	CAGT' SCCAL SCCAL SGGA(SGCAL SGAAL SCACL SCCAL
D GAT	I ATC	TACC	C TGT	TCA(TTA) TGA(TGA) TGT(TGT(CCA) CCA) CAAI

Fig. 111

2160 2318 2397 2476 2555 2634 2713 2792 2950 3029 3108 2002 2871 3424 3187 SAACTGGTCCAGCCGCCGAAGAGTAGGAAAAGGAGAAGGGCTGCTCAGGGAAACATTGGCTGGGGGCACGGAATAAGCAC **ATAGTAAAAAGGGAACATCAGGGTCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAG** IGGTGCATAAGAAAAGAGAAAAGGGTTGCCTTTTGTGTTTTGAGTAAGAATAATTAAACCATAAGGAAGACCATGTATAA CCTAGGTTTCATCATTTTTGGCTCCTTAGCATGGCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAA ATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA AAATATCAACAGAACTCTAGCCAAAGGCCAGAACTCCAGAACACAGAAAGGAAAAGGAAATCCTAATCCTTCTGTTTTGA SAAGAGAGAACTGTAGTTGCTTCACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACA ICTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCA ATGGCCTGGGGTGGGGAGTGGGGAGTAGGGAATATGTGGGATTTGGTTTAAGTTCATCATTGGGAGAGTTCCTGGA CTTAATTTCCTTACTGATAAATGGGGTAGTAATACCTATCTCAAAAAATTATTGCACATATTAAATAACATTCCTCTA ITICAATITIGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATA AAAATTTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACTTTTCATG ACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAACCCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAG <u> AAAGGCAAGAAAGAGGAAGACAAGTCTTGGAGTACCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCT</u> <u> AACTGATGGAAATAATAGTCACCAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT</u> SCAAGCCACTGAATTTGAGTTTTCACTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGT IGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT STCTCTCGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCTTTCGTGTAT IGTTCATCCAGCAACCAGGATGATCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAAAAAAGCCATGA <u> AATTNTAGCAAGCCACTGAATTTGAGTTTTCACTTTGGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCT</u>

Fig. 11J

TTCTTGGTCTTAATTTCCTTACTGATAAAATGGGGTWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACA	3582
TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAGGAGTTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAG	3661
AAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTAATA	3740
TGGGAATAAAATTTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACAC	3819
TITICATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAACCCCCATCCAACCTTAGACTCACGAACAAATCCACCT	3898
GAGATCAGCAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAAAAA	3977
AAAAAAA	3985

Fig. 11K

Fig. 11L

noventen orten

79 398	99 458	119 518	139 578	155 629	708 787 866 945 102 110 118 134
K AAA	TACT	W TGG	L		TAGC AGGA AAAA TGAG TCAA TTGG
G GGA	D I GAC ATA	R CGT	D GAT		TCTGCTCTTCTCCTTCCAACCCATCTATTCCCTATCTGTCTACCAGAGGGGACAGGAGGACTGCTTCTTTCT
K AAA	D GAC	W TGG	999		TCTAC CAGG; SACT(CTGT) CTCTC SAGAC SAGATI
C TGC	Q CAG	R AGG	P CCT	* TAG	TCTCI TTCTO GTAAO TCGTO TGGAO TGGAO TATAO
F TTT	L	K AAA	F TTT		CCTAL GCCAT GGGA GGGA CAGT CAGT CCAT
D GAC	F TTT	E GAG	Q CAG	$_{ m L}$	ATTCO SCTAO CTGAO CTGTO CTGTO CCTO
R AGG	K AAG	E GAA	P CCA	T ACC	ATCT/ SGAT(AGTA(TACT/ SGTC/ SGTC/ SGAG(CTGA/
s AGC	L CTG	R CGT G	M ATG	GGG TTC	ACCCZ SACTC CTGTZ ACCAZ CATAC AGAGC
E GAA	K AA	H CAT	N AAC	GGG	TCCAI SGGGG STATI STATI TAGCI TAGCI CAGCO
N AAT	E GAG	Y TAC	V GTG	A GCT	TTCTT CACTO STCCO CAGGA AGGGA CAGGO CTTGT
¥ GG	P CCA	I ATT	Y TAC	I ATT	rcci rctg rctg rcag sccr aagcg aaac rtcc
S A TCT T	T ACG	L TTA	K AAG	E GAG	CTTCT SAGA! STGG! STGG! CACA! AAGA!
S TCA	N AA	ე მ	9 9	P CCT	rgcrc rata(rata) ratac cargo acrco rrggi
E GAA	V GTC	I ATT	N AAT	K AAA	
S TCT	I ATT	F	${ m F}$	TACC	CTCTCACTCACTCACTCACTCACTCACTCACTCACTCAC
TACT	A GCA	Y TAT	V GTG	K AAG	TTGAC GGGAC CAAC ACAGC TTTAC CTAGC CTAGC
S TCC	$_{ m L}$	K AAG	S TCT	Q CAA	ACAC GAAA GTTG GTTG CCTC CCTT
L TTA	T ACA	E GAG	N AAC	L	SCTG SCCC STCT STCT CCAT SGGG SGAA
F F L S T S TTT TTC TTA TCC ACT TCT	G S T L A I GGA TCC ACA TTG GCA ATT	D A E K Y F I G L I Y GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC	I N N S V F N ATC AAC ACT GTG TTC AAT	G L L Q K T K P E I A GGT TTG CTT CAA AAG ACC AAA CCT GAG ATT GCT	CTCAAACGCTGACACTTGACTCTGT GGTCCTTGCCCATTTGGGAACTGA TCAGTTTTACGGAACCAACTCAGTT AGGCCTAGTCTGTTGACAGGGTTTG AAATTATAAACATTATTTAGGGATT GGGAACCCCATTCACATGCCCTCC CCTTGGGGAGGCTCCTAGTGCTGA CAGGATAGGAACCTTCTTGGAGACC
F TTT	G GGA	D GAT	IATC	G GGT	CTC GGT TCA(AGG AAA GGGZ CCT

Fig. 11M

COMPTO OF CHAPT

1814 1893 2130 2209 2288 2367 2446 2525 2604 2683 2762 2920 2999 3078 1972 2051 2841 1577 TITAAAATTITIGGATAGTCTCTTAGGCAACAATAATCACAATATATTCATCCCTTCAGTTCTGGAGAAAGCCTGATACC AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTAGAACTGGTCCAGCCGCCGAAGAG TAGGAAAAGAGAGGGCTGCTCAGGGAAACATTGGCTGGGGGCACGGAATAAGCACATAGTAAAAAAGGGAACATCAGGG TCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAGAAAGGCAAGAAAGGGAAGAAGACAA SATGCCTTTTGTGTTTTGAGTAAGAATAATTAAACCATAAGGAAGACCATGTATAAAACTGATGGAAATAATAGTCACC GGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAAAAAATATCAACAGAACTCTAGCCA AAGGCAAGCCCCAGAACTCAGACAAAAGGAAATCCTAATCCTTCTGTTTTGAGAAGAGAGAACTGTAGTTGCTTC ACTICCTATITCAIGACAGAATAACIGCAAACTITIAAGAICAGGAAAIGIAGACAICTAGIGATITICITIAGIAGACA GITTAATITCCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGA STAGGCAAGCCACTTCATTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGTCAGAGAAG <u> ACAAGATTGTTGTAAATCATATTTTTTTTACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTGGCT</u> GTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCATCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGT GGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGCCCAGCCTA GGTCAGCCAACCCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGCAGCCACCCTAGATCAGCTGA CCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTTGAGTACCTGGCTGTATTTGTTGAGTAT CACTITGTITCTAATATGCTGTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAT GGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT PAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAAT

LOWELD OF THE PRINCES

CTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCTTTCGTGTATTGTTCATCCAGCAACCAGGATGA TCTTGTTAAAACATTAAAACAGATTCTGTCAYKCTTTMAAAAAAAAAAAAAAAAGCCATGAAATTNTAGCAAGCCACTGAATTT	3315
GAGTITICACTITGGITICTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACT	3473
GATAAAATGGGGTWGTAATACCTATCTCAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA	3552
TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGSTAGA	3631
AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGT	3710
CAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGC	3789
CCAGCCTAGGTCAGCCAACCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGCAGCCTAGA	3868
TCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAAAA	3947
22252255	3958

Fig. 110

79	7		21	(')	27	ц)	33
	TTC	ტ	GGA	ပ	\mathtt{TGT}	FFISTSESSWNESRDFCKGK	AAA
CAC	SCIC	Λ	ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	D W E F Y Q A R C	AGA	ტ	GGA
CTG	rgca(Λ	GTT	Ø	GCA	×	AAA
CTG	CCCC	×	AAA	Ø	CAA	ပ	TGC
36000	3AGG(ы	CII	×	TAT	ഥ	TTT
ACGG	3AAA(\triangleright	GTG	Бч	TTT	Ω	GAC
3GAG	3GGA(\triangleright	GTA	ഥ	GAA	ഷ	AGG
CTCAC	rccac	>	GTG	M	TGG	ß	AGC
'ATT(SCCTI	\vdash	ATT	Ω	GAC	囝	GAA
4GCA1	CTA	П	CLL	×	AAA	Z	AAT
AAGG7	ZAAG(ტ	999	Д	CCC	M	TGG
SCAA	SAAGO	ഗ	ICI	Y F C P K	IGC	ഗ	$_{ m LCL}$
TGGC	CTG	Н	ATC	ഥ	TIC	ഗ	TCA
TGCI	CCAI	Н	ATC	\succ	TAT	Ы	GAA
AACGI	BACC	Σ	ATG	П	CIL	ഗ	$_{\rm ICI}$
AAGE	GAAG	M H	CAC	П	CTA	⊣	ACT
SAAGG	ACCAG	M	TGG	ഥ	TTT	ഗ	$^{\mathrm{ICC}}$
GAAG	3GCC7	N	AAC	П	TTA	ᆸ	TTA
GAGACTGTGAAGAAGGAAGGATGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCTGCCTG	AGCATTAGGCCACCAGGAAGACCCCCATCTGCAAGCAAGC	Σ	ATC ATG AAC TGG CAC ATG	M T L F L L	ACC	ഥ	$_{ m TIC}$
GAGA	AGCF		ATC	Σ	ATG	ഥ	TTT

Fig. 11P

79	99	119	139	145
398	458	518	578	599
TACT	W TGG	A GCG	I ATC	
I	R	C	R	
ATA	CGT	TGT	AGG	
D	W	N	R	
GAC	TGG	AAC	CGC	
Q CAG	R AGG	F	Y TAC	
L	K AAA	N AAT	S AGC	
F	E	Q	I	
TTT	GAG	CAG	ATC	
K	E	N	D	
AAG	GAA	AAT	GAC	
L CTG	R	Q CAG	C TGT	
K	H	N	S	
AAA	CAT	AAT	TCA	
E	Y	T	A	
GAG	TAC	ACC	GCA	
P	I	V	A	
CCA	ATT	GTT	GCT	
T	L	N	D	
ACG	TTA	AAT	GAT	
N	3	299	F	
AAC	9	880	TTT	
V	I	N	T	*
GTC	ATT	AAT	ACA	TGA
I	F	F	K	K
ATT	TTT		AAG	AAA
A	Y	V	T	A
GCA	TAT	GTG	ACA	GCC
LTTG	K	S	L	N
	AAG	TCT	CTA	AAT
T	E	N	299	K
ACA	GAG	AAC	9	AAG
S	A	N	I	E
	GCT	AAC	ATT	GAG
G	D	I	T	c
GGA	GAT	ATC	ACC	TGT

1073 1152 1231 757 915 836 994 **ICACAGTTCCCTGTGACAAGAACTATACTTGCAACTCTTTTTGAATCCATACAGGTCGTCTGGCCAATGATTCTTTTAC** CTAGCCATCTCCAGGAGACAGGATCAGTTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTAC CTAGGGAGTAACTGTAGAGTGAGAAATTATAAACATTATTTAGGGATTACCATGGTGGAAGAGGGGATAAACATAGGTCC CCTCAGTCTGAACTAAGGCTTGGCCTTGGGGAGGGCTCCTAGTGCTGAGCTTGGAGCAGCAGGACAGCAGCAGCATTGTTT **ATGGGAATGGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAGGAAG** TGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCTCCTAACTCCACAAGCGAGGGTAGCAGAGGGTTCT

Fig. 110

٠...

DOVEDING OTIPOI

CAAACACACTAGATTTCTGTTCTTCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAA	1310
ACTCCATTATAACATATGTAACTCCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTTGAGTA	1389
CCTGGCTGTATTTGTTGAGTATTTTTAAAATTTTTGGATAGTCTTTAGGCAACAATAATCACAATATTCATCCCTTC	1468
AGTICTGGAGAAAGCCTGATACCAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTA	1547
GAACTGGTCCAGCCGCCGAAGAGAGAAAAGAGAGAGGCTGCTCAGGGAAACATTGGCTGGGGGCACGGAATAAGCAC	1626
ATAGTAAAAAGGGAACATCAGGGTCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAG	1705
AAAGGCAAGAAAGAGGAAGACAAGTCTTGGAGTACCCTGGCTGTTCTCCACACACCACAAGACATCAGCTATACTCTGCT	1784
TGGTGCATAAGAAAGAGAAAAGAGACCTTTTGTGTTTTGAGTAAGAATAATTAAACCATAAGGAAGACCATGTATAA	1863
AACTGATGGAAATAATAGTCACCAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT	1942
ACATGTCATTGTATGTATACCAAACAAGATTGTTGTAAATCATATTTTTTTT	2021
CCTAGGTTTCATCATTTTTGGCTCCTTAGCATGGCCACTTACAATTTTTTAACATGAGATAACATCAGGTGTCAGAA	2100
CTTGCTTGAAGGGAATTACCAGAAGTAATTTGTGTTTGAGATGGGGTGGAAATTGGAATTATATTAGTAG	2179
ATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA	2258
AAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCTTTTGA	2337
GAAGAGAGAACTGTAGTTGCTTCACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACA	2416
TCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCA	2495
ATGGCCTGGGGTGGGGAGTGGATAAGGGAATATGTGGGATTTGGTTTAAGTTCATCATTGGGAGAGTTCCTGGA	2574
TCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAA	2653
GCAAGCCACTGAATTTGAGTTTTCACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGT	2732
CTTAATTTCCTTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAAATTTATTGCACATATTAAATAACATTCCTCTA	2811
TGTATCTCAATGGCATTAGACATTAGGAGAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCT	2890
TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATA	2969
AAAATTTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATG	3048
ACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAACCCCCATCCAACCTTAGACTCACGAACAAATCCACCTGAGATCAG	3127

Fig. 11R

Fire For or Forest

CAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAA	3206
GICTCTCGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCTTTCGTGTAT	3285
TGTTCATCCAGCAACCAGGATGATCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAAAAAAGCCATGA	3364
AATTNTAGCAAGCCACTGAATTTGAGTTTTCACTTTGGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCT	3443
TTCTTGGTCTTAATTTCCTTACTGATAAATGGGGTWGTAATACCTATCTCAAAAAATTATTGCACATATTARATAACA	3522
TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAG	3601
AAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATA	3680
TGGGAATAAAAATTTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACAC	3759
TTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAACCCCCATCCAACCCTTAGACTCACGAACAAATCCACCT	3838
GAGATCAGCAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAAAACTTATCACTGTAAAAAAAA	3917
AAAAAAA	3925

Fig. 11S

79 158	19	39 278	59 338	79	99 458
CCA	G GGA	C TGT	K AAA	T ACT	₩ TGG
CACA	V GTT	R AGA	G GGA	I ATA	R CGT
CTG	V GTT	A GCA	K AAA	D GAC	¥ TGG
CTGC	K AAA	Q CAA	C TGC	O CAG	R AGG
GCCC	L CTT	${ m Y}$	F TTT	L	K AAA
CGGG	V GTG	F TTT	D GAC	F TTT	E GAG
GAGA	V GTA	E GAA	R AGG	K AAG	E GAA
TCAG	V GTG	W TGG	S AGC	L CTG	R CGT
ATTC	I ATT	D GAC	E GAA	K AAA	H CAT
GCAT	L	K AAA	N AAT	E GAG	Y TAC
AGGA	999	P	W TGG	P CCA	I ATT
CAAA AAGC	S TCT	C TGC	S TCT	TACG	$_{ m L}$
TGGG	I ATC	F	S TCA	N AAC	g GGC
TGCI	I ATC	Y TAT		V GTC	I ATT
ACG	1 H M I G CAC ATG ATC 1	L L Y CTA CTT TAT	S E I TCT GAA	A I V	FTT
SAAG	H CAC	L CTA	T ACT	A GCA	$^{ m Y}$
SAAG	W TGG	H L	S TCC	$_{ m ITG}$	K Y F I AAG TAT TTT ATT
GAAG	GCCA N AAC L	L TTA	$_{ m L}$	T ACA	E GAG
GAGACTGTGAAGAAGGAAGAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCTGCCTG	M N ATC ATG AAC	T L ACC TTA	F L S T TTC TTA TCC ACT	S TCC	D A E GAT GCT GAG
GAG2 AGC2	ATC	M ATG	F TTT	G GGA T	D GAT

Fig. 11T

135 569

Q CAG L CTG

> A G GCT GGG

P

M. ATG

V N GTG AAC

K AAG

F

rozmete en arene

CTCAAACGCTGACACTTGACTCTGTTCTGCTCTTTCTTCTTCCAACCCATCTATTCCCTATCTGTCTACCAGTAGC	648
GGTCCTTGCCCATTTGGGAAACTGAGCTTCTTTCTTCTGCACTGGGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA	727
TCAGTTTTACGGAAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGA	908
AGGCCTAGTCTGTTGACAGGGTTTGTTTTTTTTTAGCCTCAGAGTATACCATACTACTAGGGGAGTAACTGTAGAGTGAG	882
AAATTATAAACATTATTAGGGATTACCATGGTGGAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAA	964
GGGAACCCCATTCACATGCCCCTCCTAACTCCACAAGCGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGG	1043
CCTTGGGGAGGGCTCCTAGTGCTGAGCTTGGAGCAGCACGGACAGCAGCATTGTTATGGGAATGGAGAGAGGTCTGGG	1122
CAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCCAAGGGAGCCAAACACACTAGATTTCTGTTCT	1201
TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAAACTCCATTATAACATATGTAACT	1280
CCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTTGAGTACCTGGCTGTATTTGTTGAGTATT	1359
TTTAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTTCATCCCTTCAGTTCTGGAGAAAGCCTGATACC	1438
AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTAGAACTGGTCCAGCCGCCGAAGAG	1517
TAGGAAAAGAGAGAGGCTGCTCAGGGAAACATTGGCTGGGGGCACGGAATAAGCACATAGTAAAAAAGGGAACATCAGGG	1596
TCAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAGAAAGGCAAGAAAGA	1675
GTCTTGGAGTACCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGA	1754
GATGCCTTTTGTGTTTTGAGTAAGAATAATTAAACCATAAGGAAGACCATGTATAAAACTGATGGAAATAATAGTCACC	1833
AAAGTACAGCACATACCATTTTGTGTGTCTAATAACAATGTAGCACAGTAATGACTGTACATGTCATTGTATGTA	1912
ACAAGATTGTTGTAAATCATATTTTTTTTACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGGCT	1991
CCTTAGCATGGCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTG	2070
AGTAATTTGTGTTTGAGATGGGGTGGAAATTGGAATTATATTAGTAG	2149
GGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAGGCTGAGTCTAGGTGGAGAAAAAATATCAACAGAACTCTAGCCA	2228
AAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAGAGAGAACTGTAGTTGCTTC	2307
ACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTTTTAGTAGACA	2386

Fig. 11U

First of Care

GTTTAATTTCCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCAATGGCCTGGGGTGGGAGTGGGGA	2465
GTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGT	2544
GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAA	2623
CACTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAAT	2702
GGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT	2781
TAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAAT	2860
GTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGTCAGAGAAG	2939
GGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGCCCAGCCTA	3018
GGTCAGCCAACCCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGGCGACCCTAGATCAGCTGA	3097
AACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAA	3176
CTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCTTTTGGTGTATTGTTCATCCAGCAACCAGGATGA	3255
TCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAAAAAAAAAAAGCCATGAAATTNTAGCAAGCCACTGAATTT	3334
GAGTTTTCACTTTGGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACT	3413
GATAAAATGGGGTWGTAATACCTATCTCAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA	3492
TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGSTAGA	3571
AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAATTTGTGCAAGT	3650
CAGAGAAGGGTGCCTTAAAAATGTTGTGGCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCAAATGTGGGC	3729
CCAGCCTAGGTCAGCCAACCCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCTTAGA	3808
TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAA	3887
222525555	3898

Fig. 11V

COVECTAL CALCACO

100 100 SMDY SRDF SRDF SRDF SRDF SRDF	
60 70 80 90 100	
90 	IAK IAK IAK IAK IAK
CEFFS CFFFS CFFLS CFFLS CFFLS CFFLS CFFLS CFFLS	ICEMN ICEMN ICEKN ICEKN ICEKN
80 	O SYRW SYRW SYRR SYRR SYRR E E
RANWDE RANWDE ROWEE ROWEE ROWEE ROWEE	180 ASCEVS' ASCEVS' ASCDIS' ASCDIS' ASCDIS' AGFTLE AGFTLE
TVCPI TVCPI TVCPI TVCPI TVCPI	TYDAA TYDAA TEDAA TEDAA TEDAA KPELI
70 RRSYG RRSYG RSYG RSYG RSYG	170
STMP. STMP. GFIT. GFIT.	DCVT] DCVT] NCAT] NCAT] NCAT] CDLGI GDLGI
60 SRNDE SPSPN SPSPN SPSPN SPSPN	160 DOONE DOONE DOONE DOONE TROEF
SQI FC SQI FC SQI FC FGS SS FGS SS FGS SS FGS SS	NVTNÇ NVTNÇ NVTNÇ NVTNÇ NVTNÇ KYVNN KYVNN
50 3VQNV 3VQNV 3VQNV 	150 SVFNG SVFNG SVFNG SVFNG SVFNG SVFNG SVFNG SVFNG
40 50	MINNS WINNS WINNS WINNS WINNS WINNS WINNS
40 	10
, NDGEY NDGEY NDGEY NDGEY NDGEY	140 RQPGEK YHREEK YHREEK YHREEK YHREEK YHREEK
FGKS: FGKS: FNKS: FNKS: FNKS: FNKS:	161V 161V 161I 161I 161I 161I 161I 161I
30 YEPQV YEPQI YEPQI YEPQI YEPQI	130
FFLL TFLL TFLL TFLL TFLL TFLL TFLL	DIAG: DIAG: DITD: DITD: DITD: DITD: DITD:
20 // // // // // // // // // // // // //	120
VVIK' VVIK' VVLK' VVLK' VVLK' VVLK' VVLK' VVLK' VVLK'	TPEK TPEK TPEK TPEK TPEK TPEK
10 - SGLIV SGLIV SGLIV SGLIV SGLIV SGLIV	110 LAIVN LAIVN LAIVN LAIVN LAIVN LAIVN
1	110 120 130 140 150 160 170 180 180 180 170 180 180 170 180
1	110 120 130 140 150 160 170 180 180 180 1

Fig. 11W

A GTGGTC B GTGGTC C GAGACT D GAGACT E GAGACT	10 20	20 	30 	40	50 GGGCAAAAGG GGGCAAAAGG GGGCAAAAGG	60	70 CAGGAGACGC CAGGAGACGC CAGGAGACGC CAGGAGACGC	40 50 60 70 80 90 100 1 >	90 - TGCCACACC TGCCACACC TGCCACACC TGCCACACC	100 AGCA AGCA AGCA AGCA AGCA
A TTAGG(B TTAGG(C TTAGG(D TTAGG(E TTAGG(110 120 130	120 	110 120 140 150 160 170 180 190 200 TTAGGCCACCAGGAAGACCCCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCCTGCAGCTCCTTCATCATGAACTGGCACATGATCATCT 1 </td <td>140 150 160 200 CAAGCCTAGCCTTCCAGGGAAAAGAGGCCCCTGCAGCTCCTTCATGAACTGGCACATGATCATCT CAAGCCTAGCCT</td> <td>150 AGGGAGAAAG AGGGAGAAAG AGGGAGAAAG AGGGAGAAAG</td> <td>160 </td> <td>170 AGCTCCTTC? AGCTCCTTC? AGCTCCTTC? AGCTCCTTC? AGCTCCTTC?</td> <td>180 </td> <td>190 </td> <td>200 ATCT ATCT ATCT ATCT ATCT</td>	140 150 160 200 CAAGCCTAGCCTTCCAGGGAAAAGAGGCCCCTGCAGCTCCTTCATGAACTGGCACATGATCATCT CAAGCCTAGCCT	150 AGGGAGAAAG AGGGAGAAAG AGGGAGAAAG AGGGAGAAAG	160	170 AGCTCCTTC? AGCTCCTTC? AGCTCCTTC? AGCTCCTTC? AGCTCCTTC?	180	190 	200 ATCT ATCT ATCT ATCT ATCT
A CTGGGG B CTGGGG C CTGGGG D CTGGGG	210 CTTATTGTGG CTTATTGTGG CTTATTGTGG	220 	210 220 230 240 250 260 270 280 290 300	240	250	260 TTCCCACAGA TTCCCACAGA TTCCCACAGA TTCCCACAGA	270 TTTTAACAA TTTTAACAA TTTTAACAAA 	280 	290 GTTTCACC? GGTTTCACC? GGTTTCACC?	300 CCAC CCAC CCAC CCAC

Fig. 11X-1

310	320	330	340	350	360	370	380	390	400
	_	_	_	_	_	_	_	_	
rgga.	ACAGTCTCAC	AGATTTTGG	GAGCAGTTCC	CCAAGTCCCA	ACGGCTTCAT	A CAGGAGCTATGGAACAGTCTCACAGATTTTTGGGAGCAGTTCCCCAAGTCCCAACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCAAAGAC	AGCTATGGAA	CAGTCTGCCC	CAAAGAC
TGGA	ACAGTCTCAC.	AGATTTTGG	GAGCAGTTCC	CCAAGTCCCAA	ACGCCTTCAT	B CAGGAGCTATGGAACAGTCTCACAGATTTTTGGGAGCAGTTCCCCAAGTCCCAACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCAAAGAC	AGCTATGGAA	CAGTCTGCCC	CAAAGAC
TGGA	C CAGGAGCTATGGAACAG							TCTGCCCCAAAGAC	CAAAGAC
D CAGGAGCTATGGAACAG-	4CAG		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				1	TCTGCC	-TCTGCCCCAAAGAC
								101600	-TCTGCCCCAAAGAC -TCTGCCCCAAAGAC
410	420	430	440	450	460	470	480	490	200
_	_		_	_		_	_	_	
TATC	AAGCAAGATG	TTTTTTT	TCCACTTCTG	AATCATCTTG	SAATGAAAGC	A TGGGAATTITATCAAGCAAGATGTTTTTTTTTTTCTGACTTCTTGAATCATCTTGGAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA	SCAAAGGAAA	AGGATCCACA	TTGGCAA
TTATC	AAGCAAGATG	TTTTTT	TCCACTICIG	AATCATCTTG	SAATGAAAGC	TGGGAATTTTATCAAGCAAGATGTTTTTTTTTTCTACTTCTGAATCATCTTGGAATGAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA	SCAAAGGAAA	AGGATCCACA	TTGGCAA
TTATC	AAGCAAGATG	TTTTTTP	TCCACTICIG	AATCATCTTG	SAATGAAAGC	TGGGAATTTTATCAAGCAAGATGTTTTTTTTTTCTTATCCACTTCTTGAATCAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA	SCAAAGGAAA	AGGATCCACA	TTGGCAA
TTATC	AAGCAAGATG'	TTTTTT	TCCACTTCTG	AATCATCTTG	SAATGAAAGC	TGGGAATTTTATCAAGCAAGATGTTTTTTTTTTCTTATCCACTTCTTGGAATGAAAGCAGGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA	SCAAAGGAAA	AGGATCCACA	TTGGCAA
TTATC	AAGCAAGATG'	TTTTTTP	TCCACTTCTG	AATCATCTTG	SAATGAAAGC	TGGGAATTTTATCAAGCAAGATGTTTTTTTTTTTTCTGACTTCTTGAATCATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA	SCAAAGGAAA	AGGATCCACA	TTGGCAA
LTTATC	4AGCAAGATG	TTTTTTP	NTCCACTICIG	AATCATCTTG	SAATGAAAGC	TGGGAATTTTATCAAGCAAGATGTTTTTTTTTTCTACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTTTGCAAAGGAAAAGGATCCACATTGGCAA	SCAAAGGAAA	AGGATCCACA	TTGGCAA

Fig. 11X-2

TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAACTGATGCTGAGAAGTATTTTATTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAACTGATGCTGAGAAGTATTTTATTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAACTGATGCTGAGAAGTATTTTATTGGCTTAATTTTACCATCGTGAAGAGAAAAGGTGGCG PTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAACTGATGCTGAAGTATTTTATTGGCTTAATTTACCATCGTGAAGAAAAGGTGGCG

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TTGTCAACACGCCAGAGAAACTGAAGTTTCTTCAGGACATAACTGATGCTGAGAAGTATTTTATTGGCTTAATTTACCATCGTGAAGAGAAAAGGTGGCG

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tions to the total

700	SCATCA	SCIGGG	SCATCA	SCIGGG	SCATCA	SCTGGG
069	CATTTGATGCT	AACCTGAGATT	CATTIGAIGCI	AACCTGAGATT	CATTIGAIGCI	AACCTGAGATT
089	TAACAAAGA	AAAAGACCA	TAACAAAGA	AAAAGACCA	TAACAAAGA	AAAAGACCA
670	GACCATTGGCC	TGGTTTGCTTC	GACCATTGGCC	TGGTTTGCTTC	GACCATTGGCC	TGGTTTGCTTC
099	CAACTGTGC	TGGGGATCI	CAACTGTGC	TGGGGATCI	CAACTGTGC	TGGGGATCT
650	AATCAGAATTI	CCACAGITIC	AATCAGAATTI	CCACAGTTTCC	AATCAGAATTI	CCACAGTITC
640	ACCAATCAG	GTGAACATG	ACCAATCAG	GTGAACATG	ACCAATCAG	GTGAACATG
630	ATGGCAATGT	ATGGCAAGTAC	ATGGCAATGTT	ATGGCAAGTAC	ATGGCAATGT1	ATGGCAAGTAC
620	ICTGTGTTCA	CTGTGTTCA	CTGTGTTCA	CTGTGTTCA	CTGTGTTCA	ICTGTGTTCA
610 	A ITGGATCAACACTCTGTGTTCAATGGCAATGTTACCAATCAGAATTTCAACTGTGCGACCATTGGCCTAACAAAGACATTTGATGCTGCATCA	B ITGGAICAACAACTCTGTGTTCAATGGCAAGTACGTGAACATGCCACAGTTTCCTGGGGATCTTGGTTTGCTTCAAAAGACCAAACCTGAGATTGCTGGG	C TTGGATCAACACTCTGTGTTCAATGGCAATGTTACCAATCAGAATTTCAACTGTGCGACCATTGGCCTAACAAAGACATTTGATGCTGCATCA	D TIGGATCAACAACTCTGTGTTCAATGGCAAGTACGTGAACATGCCACAGTTTCCTGGGGATCTTGGTTTGCTTCAAAAGACCAAACCTGAGATTGCTGGG	E TIGGAICAACAACTCIGIGITCAAIGGCAAIGITACCAAICAGAAITITCAACIGIGCGACCAIIGGCCTAACAAAGACAITIGAIGCIGCAICA	F TIGGAICAACACTCIGIGITCAAIGGCAAGIACGIGAACAIGCCACAGIIICCIGGGGAICTIGGIIIGCIICAAAAGACCAAACCIGAGATIGCIGGG
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	710	720	730	740	750	760	770	780	790	800
	_		_	_			_	_	_	_
Ø	A TGTGACATCAGCTACCGCAGGATCTGTGAGAAGAATGCCCAAATGATCACAGTTCCCTGTGACAAGAACTATACTTGCAACTCTTTTGAATCCATACAGG	ACCGCAGGATC	TGTGAGAAGA	ATGCCAAATGP	TCACAGTIC	CTGTGACAA	GAACTATACT	IGCAACTCTT	TTTGAATCC	ATACAGG
В	B TICACCCIGGAATAGCICAAACGCIGACACTIGACICIGIICIGCICITCICCTITCITCCAACCCAICIATIC	AGCTCAAACGC	TGACACTTGAC	CICTGITCIGC	TCTTCTCT	TCTTCCAAC	CCATCTATTC		1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1
ပ	C TGTGACATCAGCTACCGCAGGATCTGTGAGAAGAATGCCAAATGATCACAGTTCCCTGTGACAAGAACTATACTTGCAACTCTTTTTGAATCCATACAGG	ACCGCAGGATC	TGTGAGAAGA	ATGCCAAATG?	TCACAGTIC	CTGTGACAA	GAACTATACT.	IGCAACTCTT	TTTGAATCC	ATACAGG
Ω	D TICACCCIGGAATAGCICAAACGCIGACACTIGACICIGITCIGCICTICICCTITCTICCAACCCAICTAITC	AGCTCAAACGC	TGACACTTGAC	CICTGTICTGC	TCTTCTCT	TCTTCCAAC	CCATCTATIC			
[+]	E TGTGACATCAGCTACCGCAGGATCTGTGAGAAGAATGCCCAAATGATCACAGTTCCCTGTGACAAGAACTATACTTGCAACTTTTTGAATCCATACAGG	ACCECAGGATC	TGTGAGAAGA	YTGCCAAATGA	TCACAGTIC	CTGTGACAA	GAACTATACT.	IGCAACTCTT	TTTGAATCC	ATACAGG
ĮΞ·	F TTCACCCTGGAATAGCTCAAACGCTGACACTTGACTCTGTTCTGCTCTTCTTCCTTC	AGCTCAAACGC	TGACACTTGAC	CTCTGTTCTGC	TCTTCTCCT	TCTTCCAAC	CCATCTATIC		1 1 1 1 1 1 1 1 1	

810 CTGGCCA CTGGCCA	820 830 840 850 86 	A TCGTCTGGCCAATGATTCTTTTACTTACCTATCTGTCTACCAGTAGCGGTCCTTGCCCATTTGGGAAACTGAGCTTCTTTTTTGGGAAACTGAGCTTCTTTTTTGGGACTTGG	 C TCGTCTGGCCAATGATTCTTTTACTTACCTATCTGTCTACCAGTAGCGGTCCTTGCCCATTTGGGAAACTGAGCTTCTTTTTTTGGGAAACTGAGCTTCTTTTTGGGAAACTGAGCTTCTTTTTTTT	 E TCGTCTGGCCAATGATTCTTTTACTTACCTATCTGTCTACCAGTAGCGGTCCTTGCCCATTTGGGAAACTGAGCTTCTTTTTGGGAAACTGAGCTTCTTCTGCACTGGGGGACTGG	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
		CTGGCCAATGATTCTTT	TCTGGCCAATGATTCTTT	TCTGGCCAATGATTCTTT	

Fig. 11X-3

COTEST OF THE

1000	l TGAT	TGAT	TGAT	TGAT	TGAT	TGAT
		B ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTTACGGAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGA	C ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTTACGGAACAACTCAGTTAGTAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGA	D ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTTACGGAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGA	E ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTTACGGAACAACTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGA	ATGCTAGCCATCTCCAGGAGACAGGATCAGTTTTACGGAAACAACTCAGTTAGTAGAGATGAGGTCCGCTTCTGTAGTACTGAGCATTTCTGACTGA
066	 3CATT	SCATT	SCATT	SCATT	3CATT.	3CATT.
	ACTGA(ACTGA(ACTGA(ACTGA(ACTGA(ACTGA(
980	 STAGT?	STAGT?	TAGT!	STAGT?	STAGT?	STAGT?
	CTTCT(CTTCT	TTCT(CTTCT(TTCT(CTTCT
970	- STCCG(3TCCG(3TCCG(3TCCG(3TCCG(3TCCG(
	ATGAG(ATGAG(4TGAG	4TGAG(4TGAG	ATGAG(
096	l TAGAGI	ragagi	TAGAG	TAGAG i	TAGAG i	TAGAG
	TAGTA	TAGTA	TAGTA	TAGTA	TAGTA	TAGTA
950	 TCAGT	TCAGT	TCAGT	TCAGT	TCAGT	TCAGT
	ACAAC	ACAAC	ACAAC	ACAAC	ACAAC	ACAAC
940	 CGGAA	CGGAA	CGGAA	CGGAA	CGGAA	CGGAA
	TTTT	TTTTA	TTTT	TTTT	TTTT	TTTT
930	 ATCAG	ATCAG	ATCAG	ATCAG	ATCAG	ATCAG
_	ACAGG	;ACAGG	ACAGG	ACAGG	ACAGG	acage,
920	I AGGAG	'AGGAG	AGGAG	AGGAG	'AGGAG	.AGGAG
	TCTCC	TCTCC	TCTCC	NTCTCC	TCTCC	TCTCC
910	AGCC?	'AGCC?	'AGCC?	'AGCC?	'AGCC?	PAGCC?
	ATGCI	ATGC1	ATGC1	ATGC1	ATGC1	ATGC1
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1100	CATTAT	CATTAT	CATTAT	CATTAT	CATTAT	CATTAT
1090	GAAATTATAAA	GAAATTATAAA	GAAATTATAAA	GAAATTATAAA	GAAATTATAAA(GAAATTATAAA(
1080	TGTAGAGTGP	TGTAGAGTGA	TGTAGAGTGA	TGTAGAGTGA	TGTAGAGTGA	TGTAGAGTGA
1070	AGGGAGTAAC	AGGGAGTAAC	AGGGAGTAAC	AGGGAGTAAC	AGGGAGTAAC	AGGGAGTAAC
1060	CCATACTACT	CCATACTACT	CCATACTACT	CCATACTACT	CCATACTACT	CCATACTACT
1050	TCAGAGTATA	TCAGAGTATA	TCAGAGTATA	TCAGAGTATA	TCAGAGTATA	TCAGAGTATA
1040	TATTTAGCC	TATTTAGCC	TATTTAGCC	TATTTAGCC	TATTTAGCC	TATTTAGCC
1030	GGGTTTGTTT	GGGTTTGTT	GGGTTTGTTT	GGGTTTGTTT	GGGTTTGTTT	GGGTTTGTTT
1020	TCTGTTGACA	TCTGTTGACA	TCTGTTGACA	TCTGTTGACA	TCTGTTGACA	TCTGTTGACA
1010	A CAAAAAGGCCTAGTCTGTTGACAGGGTTTGTTTTTTAGCCTCAGAGTATACCATACTAGGGGGGGTAACTGTAGAGTGAGAAATTATAAACATTAT	B CAAAAAGGCCTAGTCTGTTGACAGGGTTTGTTTTTTTAGCCTCAGAGTATACCATACTAGGGGAGTAACTGTAGAGTGAGAAATTATAAACATTAT	C CAAAAAGGCCTAGTCTGTTGACAGGGTTTGTTTTTTTAGCCTCAGAGTATACCATACTACTAGGGAGTAACTGTAGAGTGAGAAATTATAAACATTAT	D CAAAAAGGCCTAGTCTGTTGACAGGGTTTGTTTTTTAGCCTCAGAGTATACCATACTAGGGGGGGTAACTGTAGAGTGAGAAATTATAAACATTAT	E CAAAAAGGCCTAGTCTGTTGACAGGGTTTGTTTTTTTAGCCTCAGAGTATACCATACTAGGGGGGGTAACTGTAGAGTGAGAAATTATAAACATTAT	F CAAAAAGGCCTAGTCTGTTGACAGGGTTTGTTTTTTAGCCTCAGAGTATACCATACTAGGGAGTAACTGTAGAGTGAGAAATTATAAACATTAT
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200 -	AAG	AAG	AAG	AAG	AAG	AAG	
⊣	CTCCAC	CTCCAC	CTCCAC	CTCCAC	CTCCAC	CTCCAC	
1190 	CCTCCTAA	CCTCCTAA	CCTCCTAA	CCTCCTAA	CCTCCTAA	CCTCCTAA	
1180	TCACATGCC	TCACATGCC	TCACATGCC	TCACATGCC	TCACATGCC	TCACATGCC	
. 1170	AGGGAACCCCAT	AGGGAACCCCAI	AGGGAACCCCAT	AGGGAACCCCAT	AGGGAACCCCAT	AGGGAACCCCAT	
1160	CTGTTCTCA	CTGTTCTCA	CIGITCICA	CTGTTCTCA	CTGTTCTCA	CTGTTCTCA	
1150 	GACTTCGTCT	GACTTCGTCT	GACTTCGTCT	GACTTCGTCT	GACTTCGTCT	GACTTCGTCT	
1140	raggiccigi	PAGGTCCTGI	raggreergi	raggreergi	raggreergi	PAGGTCCTGT	
1130 	GGGATAAACA1	GGGATAAACAI	GGGATAAACA	GGGATAAACA	GGGATAAACA	GGGATAAACA	
1120	IGGTGGAAGA	IGGTGGAAGA	IGGTGGAAGA	IGGTGGAAGA	IGGTGGAAGA	IGGTGGAAGA	
1110	A TTAGGGATTACCATGGTGGAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCTCCTAACTCCACAAG	B TTAGGGATTACCATGGTGGAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCTCCTAACTCCACAAG	C TTAGGGATTACCATGGTGGAGAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCTCCTAACTCCACAAG	D TTAGGGATTACCATGGTGGAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCTCCTAACTCCACAAG	E TTAGGGATTACCATGGTGGAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCTCCTAACTCCACAAG	F TTAGGGATTACCATGGTGGAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAAGGGAACCCCATTCACATGCCCCTCCTAACTCCACAAG	
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Fig. 11X-4

1300	GTTTAT	GTTTAT	GTTTAT	GTTTAT	GTTTAT
1290 	SACAGCAGCAT!	ACAGCAGCAT!	SACAGCAGCATI	SACAGCAGCATI	SACAGCAGCAT
1280	AGCAGCACG	AGCAGCACG(AGCAGCACG	AGCAGCACG	AGCAGCACG
1270	CTGAGCTTGG	CTGAGCTTGG	CTGAGCTTGG	CTGAGCTTGG	CTGAGCTTGG
1260	GCTCCTAGTG	GCTCCTAGTG	GCTCCTAGTG	GCTCCTAGTG	GCTCCTAGTG
1250 	CTTGGGGAGG	CTTGGGGAGG	CTTGGGGAGG	CTTGGGGAGG	CTTGGGGAGG
1240	PAGGCTTGGC	PAGGCTTGGC	PAGGCTTGGC	PAGGCTTGGC	AAGGCTTGGC
1230	AGTCTGAACT	AGTCTGAACT	AGTCTGAACT	AGTCTGAACT	AGTCTGAACT
1220	GGCTCTCCTC	GGCTCTCCTC	GGCTCTCCTC	GGCTCTCCTC	GGCTCTCCTC
1210	A CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGGCCTTGGGGAGGGCTCCTAGTGCTGAGCTTGGAGCAGCAGGACAGCAGCATTGTTTAT B. CGAGGGTAGCAGAGGCTCTCTCTCAACTAAGACTAAGGCTTGGCCTTGGGGAGGGCTCCTAGTGCTGAGCTTGGAGCAGCACGGACAGCAAGCA	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGGCCTTGGGGAGGCCTCCTAGTGCTGAGCTTGGAGCAGGACGGAC	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGGCCTTGGGGAGGCTCCTAGTGCTGAGCTTGGAGCAGCAGGACAGCAGCATTGTTAT	CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGGCGAGGGCTCCTAGTGCTGAGCTTGGAGCAGCAGCAGGACAGCAGCAGCATGTTTAT	F CGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGGCCTTGGGGAGGGCTCCTAGTGCTGAGCTTGGAGCAGCAGGACAGCAGCAGCATTGTTAT
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	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
	_	_	_		_	_	_	_	_	_
¥	A GGGAATGGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAGGGAGCCAAACAACACTAGATTTCTGTTCT	SGTCTGGGCAG	GATAGGAACC	TTCTTGGAGA	CCCCTTTGA	GAAAACCAG	SCAGCCAAGGG	agccaaaca.	CACTAGATTT	TGTTCT
Д	B GGGAATGGAGAGGCTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAGGGAGCCAAACAACACTAGATTTCTGTTCT	SGTCTGGGCAG	GATAGGAACC	TTCTTGGAGA	CCCCTTGAZ	GAAAACCAG	SCAGCCAAGGG	agccaaaca.	CACTAGATTT	TGTTCT
ပ	C GGGAATGGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAGGGAGCCAAACAACACTAGATTTCTGTTCT	SGTCTGGGCAG	GATAGGAACC	TTCTTGGAGA	ACCCCTTTGA!	GAAAACCAG	SCAGCCAAGGG	agccaaaca.	CACTAGATTT	TGTTCT
Ω	D GGGAATGGAGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCCAAGGGAGCCAAACAACACTAGATTTCTGTTCT	SGTCTGGGCAG	GATAGGAACC	TTCTTGGAGA	CCCCTTTGAZ	GAAAACCAG	SCAGCCAAGGG	agccaraca.	ACTAGATTT(TGTTCT
ŒĴ	E GGGAATGGAGAGGCTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAGGGAGCCAAACAACACTAGATTTCTGTTCT	SGTCTGGGCAG	GATAGGAACC	TTCTTGGAGA	CCCCTTTGAZ	GAAAACCAG	SCAGCCAAGGG	AGCCAAACA	CTAGATTI	TGTTCT
ĹΞι	F GGGAATGGAGAGGTCTGGGCAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAAACCAGGCAGCCAAGGGAGCCAAACACACAC	GTCTGGGCAG	GATAGGAACC	TTCTTGGAGA	CCCCTTTGAR	GAAAACCAG	SCAGCCAAGGG	AGCCAAACA	CACTAGATTT	TGTTCT

1410	1420	1430	1440	1450	1460	1470	1480	1490	1500
_	_	_		_	_	_	_	_	_
A TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAAACTCCATTATAACATATGTAACTTCTTTGTAACCAAAATTTAGG	GAAGAGACACT	TAAGCTAAA	AATTCCCTTG1	CATATTTCT(SAAACTCCAT	TATAACATAT G	TAACTCCTT	TGTAACCAAA	ATTTAGG
B TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAAACTCCATTATAACATATGTAACTTCTTTGTAACCAAAATTTAGG	GAAGAGACACT	TAAGCTAAA	AATTCCCTTG1	CATATTTCT(SAAACTCCAT	PATAACATAT G	TAACTCCTT	TGTAACCAAA	ATTAGG
C TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAAACTCCATTATAACATATGTAACTTCTTTGTAACCAAAATTTAGG	GAAGAGACACT	TTAAGCTAAA	AATTCCCTTG1	CATATTTCT	SAAACTCCAT	TATAACATATG	TAACTCCTT	TGTAACCAAA	ATTAGG
D TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAAACTCCATTATAACATATGTAACTCCTTTGTAACCAAAATTTAGG	GAAGAGACACT	TAAGCTAAA!	AATTCCCTTG1	CATATTTCT(SAAACTCCAT	TATAACATAT G	TAACTCCTT	TGTAACCAAA	ATTTAGG
E TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTTCTGAAACTCCATTATAACATATGTAACTTCTTTGTAACCAAAATTTAGG	GAAGAGACACT	TTAAGCTAAA	AATTCCCTTG1	CATATTTCT	SAAACTCCAT	TATAACATAT G	TAACTCCTT	IGTAACCAAA	ATTTAGG
F TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCCTTGTCATATTCTGAAACTCCATTATAACATATGTAACTCCTTTGTAACCAAAATTTAGG	GAAGAGACACT	TTAAGCTAAA	AATTCCCTTG1	CATATITCIC	SAAACTCCAT	IATAACATAT G	TAACTCCTT	IGTAACCAAA	ATTAGG

1900		STICICC	STICICC	STICICC	STICICC	STICICC	STICICC
1890	_	STACCCTGGCT	STACCCTGGCT	STACCCTGGCT	STACCCTGGCT	STACCCTGGCT	STACCCTGGCT
1880	_	AAGTCTTGGA	AGTCTTGGA(AGTCTTGGA(AGTCTTGGA(AAGTCTTGGA(AAGTCTTGGA(
1870	_	4GAGGAAGAC <i>I</i>	AGAGGAAGAC	AGAGGAAGAC	AGAGGAAGAC <i>I</i>	AGAGGAAGAC <i>I</i>	agaggaagac <i>i</i>
1860	_	AAGGCAAGAAI	AAGGCAAGAAI	AAGGCAAGAA	AAGGCAAGAAI	AAGGCAAGAAI	AAGGCAAGAAI
1850		CACTGGAAGA	CACTGGAAGA	CACTGGAAGA	CACTGGAAGA	CACTGGAAGA	CACTGGAAGA
1840	_	CATTTGGCCA	CATTTGGCCA	CATTTGGCCA	CATTTGGCCA	CATTTGGCCA	CATTTGGCCA
1830		ACAGGGAGTI	ACAGGGAGTT	ACAGGGAGTT	ACAGGGAGTT	ACAGGGAGTT	ACAGGGAGTI
1820		GAGACAGGAAI	GAGACAGGAA	GAGACAGGAA	GAGACAGGAA	GAGACAGGAA	GAGACAGGAA
1810		A IGGAAAICACCIGAGACAGGAAACAGGGGGITCAITIGGCCACACIGGAAGAAGGCAAGAAAGAGGGAAGACAAGICTIGGAGIACCCIGGCIGIICICC	B TGGAAATCACCTGAGACAGGAAACAGGGGGGTTCATTTGGCCACACTGGAAGAAAGGCAAGAAAGA	C TGGAAATCACCTGAGACAGGAAACAGGGGGGTTCATTTGGCCACACTGGAAGAAAGGCCAAGAAAGA	D TGGAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAGAAAGGCAAGAAAGA	E TGGAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAGAAAGGCAAGAAAGA	F TGGAAATCACCTGAGACAGGAAACAGGGAGTTCATTTGGCCACACTGGAAGAAAGGCAAGAAGAGGGAAGACAAGTCTTGGAGTACCCTGGCTGTTCTCC
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2000	AAGAC	PAGAC	AAGAC	AAGAC	AAGAC	AAGAC
1990 	TAAACCATAAGG	TAAACCATAAGG	TAAACCATAAGG	TAAACCATAAGG	TAAACCATAAGG	TAAACCATAAGG
1980	TAAGAATAAT	TAAGAATAAT	TAAGAATAAT	TAAGAATAAT	TAAGAATAAT	TAAGAATAAT
1970 	GTGTTTGAG	GTGTTTGAG	GTGTTTGAG	GTGTTTGAG	GTGTTTGAG	GTGTTTTGAG
1960	GATGCCTTTT	GATGCCTTTT	GATGCCTTTT	GATGCCTTTT	GATGCCTTTT	GATGCCTTTT
1950 	AGAGAAAAGA	AGAGAAAAGA	AGAGAAAAGA	AGAGAAAAGA	AGAGAAAAGA	AGAGAAAGA
1940 	TGCATAAGAA	TGCATAAGAA	TGCATAAGAA	TGCATAAGAA	TGCATAAGAA	TGCATAAGAA
1930 	CTCTGCTTGG	CTCTGCTTGG	CTCTGCTTGG	CTCTGCTTGG	CTCTGCTTGG	CTCTGCTTGG
1920	ATCAGCTATA	ATCAGCTATA	ATCAGCTATA	ATCAGCTATA	ATCAGCTATA	ATCAGCTATA
1910	A ACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGA	B ACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGA	C ACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGA	D ACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGA	E ACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGA	F ACACTCACAAGACATCAGCTATACTCTGCTTGGTGCATAAGAAAGA

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AIAGICACCA
GALGGAAALA
C CAIGIAIAAAACIGAIGGAAAIAAIAAIGACCCAAAGIACAGCACAITIIGIGICIAAIAACAAIGIAGCACAGIAAIGACIGIACAIGIGI

E CATGTATAAAACTGATGGAAATAATAGTCACCAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGTACATGTCATTGT
F CATGTATAAAACTGATGGAAATAATAGTCACCAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGTACATGTCATTGT

Leuu CCACAAT CCACAAT TCACAAT TCACAAT	1700
1590 	1690
1580	1680
1570 AATTTTGGATZ AATTTTGGATZ AATTTTGGATZ AATTTTGGATZ	1670
1560 	7
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1540	JACCIGGCI
1530 AGGTTTTGAG AGGTTTTGAC AGGTTTTGAC	AAGG'I'TTTGAU
1520 TTTGCTCTGA TTTGCTCTGA	TTTGCTCTG#
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1690 	CATTGATCT/ CATTGATCT/ CATTGATCT/ CATTGATCT/ CATTGATCT/	•
1680 	ATTGGCATCA ATTGGCATCA ATTGGCATCA ATTGGCATCA ATTGGCATCA	
1670	SCCTGGCACTG SCCTGGCACTG SCCTGGCACTG GCCTGGCACTG	
1660	ACCCCAAGGA ACCCCAAGGA ACCCCAAGGA ACCCCAAGGA	
1650	DAGCCTACTG CAGCCTACTG CAGCCTACTG CAGCCTACTG CAGCCTACTG	
1640	ATACCAGGCA(ATACCAGGCA ATACCAGGCA ATACCAGGCA ATACCAGGCA	
1630	I AGAAAGCCTG AGAAAGCCTG AGAAAGCCTG AGAAAGCCTG	
1620	CAGTTCTGGA CCAGTTCTGGA CCAGTTCTGGA TCAGTTCTGGA TCAGTTCTGGA	
1610	A ATATTCATCCCTTCAGTTCTGGAGAAAGCCTGATACCAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTAGAACTGG B ATATTCATCCCTTCAGTTCTGGAGAAAGCCTGATACCAGGCACAGGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATTGATCTAGAACTGG C ATATTCATCCTTCAGTTCTGGAGAAAGCCTGATACCAGGCACAGGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTAGAACTGG D ATATTCATCCTTCAGTTCTGGAGAAAGCCTGATACCAGGCACAGGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTGATCTAGAACTGG E ATATTCATCCTTCAGTTCTGGAGAAAGCCTGATACCAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACGCATCACTTGATCTAGAACTGG E ATATTCATCCTTCAGTTCTGGAGAAAGCCTGATACCAGGCACAGCCTACTGACCCCAAGGAGCCTGGCACGCATCACTTGATCTAGAACTGG	בבבביים דעוע
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TCCAGCCGCCGAAGAGAAAAGAGAAAGGGCTGCTCAGGGAAACATTGGCTGGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGGTCAAA ICCAGCCGCCGAAGAGAAAAGAGAAAGGGCTGCTCAGGGAAACATTGGCTGGGGGCCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGGTCAAA TCCAGCCGCCGAAGAGAAAAAGAGAAAGGGCTGCTCAGGGAAACATTGGCTGGGGGCCACGGAATAAGCACATAAAAAAGGGAACATCAGGGTCAAA B TCCAGCCGCCGAAGAGAAAAGAGAAAGGGCTGCTCAGGGAAACATTGGCTGGGGGCCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGGTCAAA TCCAGCCGCCGAAGAGAAAAGAGAAAGGGCTGCTCAGGGAAACATTGGCTGGGGGCCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGGTCAAA A TCCAGCCGCCGAAGAGAGAAAGAGAGAGGCTGCTCAGGGAAACATTGGCTGGGGGCCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGGTCAAA

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22	AGCA	AGCA	AGCA	AGCA	AGCA
	CCTT			CCTT	CCTT
2190	וקפרו ופפנו	֓֞֝֜֜֜֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	1995 1960	GGCT	1GGC1
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2180	ATCA:	ATCA FOTE	ATCA!	ATCA	ATCA
2	TTTC		TITC	TTTC.	TTTC
0 -	TAGG	J.A.G.	TAGG	TAGG	TAGG
2170	ATTCC		ATTC	ATTC	ATTC
	CTGC			CTGC.	CTGC
2160	GCTT		GCTT	GCTT	GCTT
	TLCI		STICE	TTCI	TLCI
2150 	CTAA(CTAA(CTAA(CTAA(CTAA(
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0 -	TTAC	TIAC	TTAC	TTAC	TTAC
2140	TTTA	TITA	TTTA	TTT	TTT
	TTTT.	AIII THT	ATTT.	ATTT	'ATTT
2130	ATCAT	ATCAT	ATCAT	ATCAI	ATCAT
	STAA!	STAAL	STAA	STAA!	GTAA1
2120	TGTT(Lell	TGTT	TGTT(TGTT(
21	AGAT	AGAT	AGAT	AGAT	AGAT
	AAACA	AACA GAACA	AAACA	AAACA	AAACA
2110	PACC?		FACCE	TACC?	racc?
	A ATGTATACCAAACAAGATTGTTGAAATCATATTTTTTTTACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTGGCTCCTTAGCATG	B ATGIATACCAAACAAGATIGITGITGIAAAICATATITITITATTACAACACITCIGCITCIGCATICCIAGGITTCATCATTTTTGGCTCCTTAGCATG	O AIGIAIACCAAACAAGAIIGIIGIAAAICAIAIIIIIIIAIIACAACACIAAGIICIGCIICIGCAIICCIAGGIIICAICAIIIIIGGCICCIIAGCAIG D AIGIAIACCAAACAAGAIIGIIGIAAAICAIAITIITAITACAACACIAAGIICIGCIICIGCAIICCIAGGIIICAICAITIIIIGGCICCIIAGCAIG	E ATGTATACCAAACAAGATTGTTGTAAATCATATTTTTTTT	F ATGTATACCAAACAAGATIGTTGTAAATCATATTTTTTTATTACAACACTAGGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTTGGCTCCTTAGCATG
	AA	א ל	Z D Z	EA	FA

2210		B GCCACTTACAATTTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTG	D GCCACTTACAATTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTG	E GCCACTTACAATTTTTAACATGAGATAACACATCAGGTGTCAGAACTTGCTTG	7 ないなまましなことが ほ
2220	 TTTTTAACATG	TTTTTAACATG	IIIIIAACAIG TTTTTAACAIG	TTTTTAACATG	F CONTRACTS THE THE TRACT TO A CALCACT TO A CONTRACT A CALCACT TO A CA
2230	 AGATAACACA	AGATAACACA	AGATAACACA	AGATAACACA	A C A A A A A A A A A
2240	 TCAGGTGTCA	TCAGGTGTCA	TCAGGTGTCA	TCAGGTGTCA	マン山で山でででした
2250	 GAACTTGCTT	GAACTTGCTT	GAACTIGCTT	GAACTIGCTI	゚゙゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚゚
2260	 GAAGGGAATT	GAAGGGAATT	GAAGGGAATT	GAAGGGAATT	上 なるここごとない
2270	 ACCAGAAGTA	ACCAGAAGTA	ACCAGAAGIA ACCAGAAGIA	ACCAGAAGTA	CTOCCOCTO
2280	 ATTTGTGTTT	ATTIGIGITI	AIIIGIGIII ATTTGTGTTT	ATTIGIGTTT	<u>Պ Դ Գ Դ Դ Դ Դ Դ Դ Դ Դ Դ Դ Դ Դ Դ Դ Դ Դ Դ </u>
2290	 GAGATGGGGT	GAGATGGGGT	GAGATGGGGT	GAGATGGGGT	正じじしじ 山 化じんじんじ
2300	 GGAAATT	GGAAATT	GGAAATT	GGAAATT	中中でででい

2400	_	GTGG
2390	_	AAGTICTCTGACTGTGGGAAAGGATAAGTGCTACCGTTGAGAAGGAAG
2380	_	AAGGGAAGAA
2370	_	PACCGTTGAG
2360	_	GGATAAGTGC
2350	_	TGTTGGGAAA
2340		TCTCTGACTG
2330		GGAGATACAAGT
2320	_	TAGCCGGTGG
2310	_	GGAATTATTAGTAGCCGGTGGAGATACA

GGAATTATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG

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GGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG

GGAATTATATTAGTAGCCGGTGCAGATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGG

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	A AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCCTTCTGTTTTGAGAAGAGAGAG	C AGAAAAATATCAACAGAACTCTAGCCAAAGGCCAAAGCCCCAGAACTCAGACAACAAGAAAAGGAAATCCTACTTTTGAAAAAAAA	D AGAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCTTTTGAGAAGGAGAGAGA	E AGAAAAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAACAGAAAGGAAATCCTAATCTTTTGAGAAGGAAG	F AGAAAAATATCAACAGAACTCTAGCCCAAAGGCCCCCAGAACTCAGACAACAAGGAAAGGAAATCCTAATTCTTTTGAGAAGAAGAGAGAG
2490 	GAGA	GAGA	GAGA	GAGA	GAGA
	AGAA	AGAA	AGAA	AGAA	AGAA
2480	TTTG	TTTG	TTTG	TTTG	TTTG
24	CTGT	CTGT	CTGT	CIGI	CIGI
_	CCTT	CCTT	CCTT	CCTT	CCTT
2470	TAAT	TAAT	TAAT	TAAI	TAAT
	AATCC	AATCC	AATCO	AATC(AATCO
2460 	AGGAZ	AGGA/	AGGA4	AGGA1	1GGA2
2,	AGAA7	1GAA1	4GAA1	4GAA1	4GAA1
0 –	CAAC	CAAC	CAAC	CAAC	CAACI
2450	CAGA(CAGA	CAGA(CAGA(CAGA(
	AACT(AACT	AACT(AACT(AACT
2440	CCAG	CCAG	CCAG	CCAG	CCAG
7	AGCC	AGCC	AGCC	AGCC	AGCC
0 —	GGCA	GGCA	GGCA	GGCA	GGCA
2430	CAAA	CAAA	CAAA	CAAA	CAAA
	TAGC	TAGC	TAGC	TAGC	TAGC
2420 	ACTC	ACTC	ACTC	ACTC	ACTC
2	CAGA	CAGA	CAGA	CAGA	CAGA
0 —	TCAP	TCAA	TCAA	TCAA	TCAA
2410 	AATA	AATA	AATE	AATE	AATE
	GAAA	GAAA	IGAA	IGAA	\GAAP
	A A	C Z	D 7	E 7	Ŧ

2510	2520	2530	2540	2550	2560	2570	2580	2590	2600
_	_		_			_	_		_
A TGCTTCACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCCA	TATTCATGACA	GAATAACTG(CAAACTTTTAA	GATCAGGAAA	ATGTAGACAT	CTAGTGATTTC	TTTAGTAGA	CAGTTTAATT	CCCCCA
B TGCTTCACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTTAGTAGACAGTTTAATTTCCCCCCA	ATTTCATGACA	GAATAACTG(CAAACTTTTAA	GATCAGGAA?	ATGTAGACAT	CTAGTGATTTC	TTTAGTAGA	CAGTTTAATT	CCCCCA
C TGCTTCACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTTTTTAGTAGACAGTTTAATTTCCCCCA	ATTTCATGACA	GAATAACTG	CAAACTTTAA	GATCAGGAAI	ATGTAGACAT	CTAGTGATTTC	TTAGTAGA	CAGTTTAATT	CCCCCA
D TGCTTCACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCCA	TATTTCATGACA	GAATAACTG	CAAACTTTTAA	GATCAGGAA	ATGTAGACAT	CTAGTGATTTC	TTTAGTAGA	CAGTTTAATT	CCCCCA
E TGCTTCACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA	'ATTTCATGACA	GAATAACTG	CAAACTTTAA	GATCAGGAAI	ATGTAGACAT	CTAGIGATITC	TTTAGTAGA	CAGTTTAATT	CCCCCA
F TGCTTCACTTCCTATTTCATGACAGAATAACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACAGTTTAATTTCCCCCA	TATTTCATGACA	GAATAACTG	CAAACTTTAA	GATCAGGAAA	ATGTAGACAT	CTAGTGATTTC	TTTAGTAGAC	CAGTTTAATT	CCCCCA

2700	_	AAGTTCA
2690	_	SATTIGGTIT
2680		SAATATGTGG
2670		GTAGATAGGG
2660		GGAGTGGGGA
2650	_	GCCTGGGGTG
2640	_	<u> AAAGGAGCCCCAATGGCCTGGGGTGGGAGTGGGGAGTAGGGGAATATGTGGGATTTGGTTTAAGTTCA</u>
2630		GTTCTAAAAG
2620		TTCTGTGCAG
2610		AGATTAGGAGACACTTCTGTGCAGGTTCTA
		A.

AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCAATGGCCTGGGGTGGGGAGTGGGGAGTAGAGAAAATATGTGGGATTTGGTTTAAGTTCA AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGGAGTGGGGAGTAGGGAATATGTGGGATTTGGTTTAAGTTCA AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCAATGGCCTGGGGTGGGGAGTGGGGAGTAGGGAATATGTGGGATTTGGTTTAAGTTCA ක **ට**

AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGGAGTGGGGAGTAGGGAATATGTGGGATTTGGTTAAGTTCA AGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCCAATGGCCTGGGGTGGGGAGTGGGGAGTAGGGAATATGTGGGATTTGGTTAAGTTCA

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2800	A TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAA	B TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAA	C TCATTGGGAGAGTICCTGGATCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAA	D TCATTGGGAGAGTICCTGGATCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAA	E TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAA	F TCATTGGGAGAGTTCCTGGATCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAA
	AAA1	LAAA 1	AAA1	AAA1	AAA1	AAA1
2790 I	ATG	ATG	ATG	ATG	ATG	ATG
27	1399y	GGCP	1399y	1399y	GGCP	1GGC
	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA
2780 	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA
	TTAA	TTAA	TTAA	TTAA	TTAA	TTAA
2770 I	GCTT	GCTT	GCTT	GCTT	GCTT	GCTT
27	GCAT	GCAT	GCAT	GCAT	GCAT	GCAT
	AGTG	AGTG	AGTG	AGTG	AGTG	AGTG
2760 	TAGC	TAGC	TAGC	TAGC	TAGC	TAGC
	IAGA	TAGA	TAGA	TAGA	TAGA	IAGA
09	LTAL	LTAL	LTAT	LTAT	LTAT.	LTAT
2750 I	ATCT.	YICT.	ATCT.	ATCT.	ATCT.	ATCT
	GTG2	'GTG	'GTG	'GTG	'GTG	'GTG
2740 	'AAA'	'AAA'	'AAA	'AAA'	'AAA'	'AAA1
7	AGAT	AGAT	AGAT	'AGAT	'AGAT	'AGA'I
0 —	GCTT	GCTT	GCTT	GCTT	GCTT	GCTT
2730	GCAA	GCAA	GCAA	GCAA	GCAA	GCAA
	CCTT	CCTT	CCTT	CCTT	CCTT	CCTT
2720 	GGAT	GGAT	GGAT	GGAT	GGAT	GGAT
7	ICCL	ICCL	ICCL	ICCT	ICCT	ICCT
o –	3AGT	3AGT	SAGT	SAGT	3AGT	3AGT
2710	3GGA(3GGA(3GGA	3GGA	3GGA	3GGA
	CATT(CATT(CATT	CATT	CATT	CATT
	A T(B T($^{\circ}$	D T(E T	F T(

CAAGCCACTGAATTTGAGTTTTCACTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA CAAGCCACTGAATTTGAGTTTTCACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA CAAGCCACTGAATTTGAGTTTTCACTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA CAAGCCACTGAATTTGAGTTTTCACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA CAAGCCACTGAATTTGAGTTTTCACTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA CAAGCCACTGAATTTGAGTTTTCACTTTGTTTCTAATATGCTGTGAATCAGTACAGTTTTCTTACCCTTTCTTGGTCTTAATTTCCTTACTGATAAAA 2890 2880 2870 2860 2850 2840 2830 2820 2810 മ ပ

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TGGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGA TGGGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCCAATGGCATTAGACATTAGGAGAAGCATTTGTGGA TGGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAAGAAGCATTTGTGGA TGGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAAGAAGCATTTGTGGA TGGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTGTGGA ပ

Fig. 11X-10

TGGGGTAGTAATACCTATCTCAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTGTGGA

3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
_		_	_	_		_	_		_
A GGATTTGAAG	A GGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATT	rccaagaagtag	SCTTTTCAATI	TGCTAGAAGC	TTAATGTAG	SCAAGCCACTT	CATTTTCAC	SAACTTGTTI	ACTCATT
B GGATTTGAAG	B GGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTCAGAACTTGTTTACTCATT	PCCAAGAAGTA C	SCTTTTCAATI	TGCTAGAAGC	TTAATGTAG	SCAAGCCACTT	CATTTTCAC	SAACTTGTTI	ACTCATT
C GGATTTGAAG	C GGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATT	ICCAAGAAGTA (SCTTTTCAATT	TGCTAGAAGC	TTAATGTAG	SCAAGCCACTT	CATTTTCAC	SAACTTGTTT	ACTCATT
D GGATTTGAAG	D GGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATT	CCAAGAAGTA C	SCTTTTCAATI	TGCTAGAAGC	TTAATGTAG	SCAAGCCACTT	CATTTTCAC	SAACTIGITI	ACTCATT
E GGATTTGAAG	E GGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATT	ICCAAGAAGTA C	SCTTTTCAATI	TGCTAGAAGC	TTAATGTAG	SCAAGCCACTT	CATTTTCA(SAACTTGTTI	ACTCATT
F GGATTTGAAG	F GGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATT	rccaagaagta(SCTTTTCAATI	TGCTAGAAGC	TTAATGTAG	SCAAGCCACTT	CATTTTCAC	SAACTTGTTT	ACTCATT

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3190	ACACTTTTCAT
3180	ATCAAAGAC?
3170	GCCACATGAG
3160 	TTGTGGCCAA
3150	CTTAAAAATG
3140 AGAAGGGTGC AGAAGGGTGC AGAAGGGTGC AGAAGGGTGC	AGAAGGGTGC
3130	TGCAAGTCAG
3120 	TAAAAATTTG
3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3200 3200 3110 3180 3190 3200 3200	F TATAATATGGGAATAAAAATTTGTGCAAGTCAGAGAAGGGTGCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACACTTTTCATGACCTCA

A AATGIGGGCCCAGCCTAGGICAGCCAACCCCCAICCAACCCITAGACICACGAACAAAITCCACCIGAGAICAGCAGAGCCACCCTAGAICAGCIGAAACI E AATGTGGGCCCCAGCCTAGGTCAGCCCAACCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGACCACCCTAGATCAGCTGAAACT AATGTGGGCCCAGCCTAGGTCAGCCCAACCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGGCCAGCCTAGATCAGCTGAAACT B AATGTGGGCCCAGCCTAGGTCAGCCCAACCCCATCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGGCCACCCTAGATCAGCTGAAACT 3250 3230

3400		GGCCTTC	GGCCTTC	GGCCTTC	GGCCTTC	GGCCTTC	GGCCTTC
3390	_	AATCTCCATCT	AATCTCCATCT	AATCTCCATCT	AATCTCCATCT	AATCTCCATCT	AATCTCCATCT
3380		'AACTGATGC	AACTGATGC.	AACTGATGC.	'AACTGATGC	AACTGATGC	AACTGATGC
3370	_	AGCAAAATCT	AGCAAAATCT	AGCAAAATCT	AGCAAAATCT	AGCAAAATCT	AGCAAAATCT
3360		TCTCTCGTAT	TCTCTCGTAT	TCTCTCGTAT	TCTCTCGTAT	TCTCTCGTAT	TCTCTCGTAT
3350		AAAAAAAAG	AAAAAAAAG	AAAAAAAAG	AAAAAAAAG	AAAAAAAAG	AAAAAAAAG
3340	_	AAAAAAAAA	чалалалала	чаааааааа	чааааааааа	чаааааааа	AAAAAAAAA
3330	_	ATCACTGTAA?	ATCACTGTAA	ATCACTGTAA?	ATCACTGTAA?	ATCACTGTAA	ATCACTGTAA?
3320	_	ATAAAAACTTI	ATAAAAACTT7	ATAAAAACŢT?	ATAAAAACTT1	ATAAAAACTT	ATAAAAACTT
3310	_	A CTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAAAAA	B CTAAGCACAAAAATAAAAAACTTATCACTGTAAAAAAAAA	C CTAAGCACAAAAATAAAAAACTTATCACTGTAAAAAAAAA	D CTAAGCACAAAAATAAAAAACTTATCACTGTAAAAAAAAA	E CTAAGCACAAAAATAAAAAACTTATCACTGTAAAAAAAAA	F CTAAGCACAAAAATAAAAAACTTATCACTGTAAAAAAAAA

3410	3420	3430	3440	3450	3460	3470	3480	3490	3500
	_	_	_	_	_	_	_	_	_
A ATCCTTCTCCCTTTATTGTCCTTTTCGTGTTTTTTTCATCCAGCAACCAGGATGATCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAA	TATTGTCCTTI	CGTGTATTG	TTCATCCAGCA	ACCAGGATG	ATCTTGTTAA.	AACATTAAAC?	GATTCTGTC	AYKCTTTMAA	AAAAAA
B ATCCTICTCCCTTTATTGTCCTTTCGTGTATTGTTCATCCAGCAACCAGGATGATCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAA	TATTGTCCTTI	CGTGTATTG	TTCATCCAGCA	ACCAGGATG	ATCTTGTTAA.	AACATTAAAC?	GATTCTGTC	AYKCTTTMAA	AAAAAA
C ATCCTTCTCCCTTTATTGTCCTTTCGTGTATTGTTCATCCAGCAACCAGGATGATCTTGTTAAAACATTAAACAGTTCTGTCAYKCTTTMAAAAAAAA	TATTGTCCTTI	CGTGTATTG	TTCATCCAGCA	ACCAGGATG	ATCTTGTTAA	AACATTAAAC?	GATTCTGTC	AYKCTTTMAA	AAAAAA
D ATCCTICTCCCTTTATTGTCCTTTCGTGTATTGTTCATCCAGCAACCAGGATGATCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAA	TATTGTCCTTI	CGTGTATTG	TTCATCCAGCA	ACCAGGATG	ATCTTGTTAA	AACATTAAAC?	GATTCTGTC	AYKCTTTMAA	AAAAAA
E ATCCTTCTCCCTTTATTGTCCTTTCGTGTATTGTTCATCCAGCAACCAGGATGATCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAA	TATTGTCCTTI	CGTGTATTG	TTCATCCAGCA	ACCAGGATG	ATCTTGTTAA	AACATTAAAC?	GATTCTGTC	AYKCTTTMAA	AAAAAA
F ATCCTTCTCCCTTTATTGTCCTTTTCGTGTATTGTTCATCCAGCAACCAGGATGATCTTGTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAA	TATTGTCCTTI	CGTGTATTG	TTCATCCAGCA	ACCAGGATG	ATCTTGTTAA	AACATTAAACE	GATTCTGTC	AYKCTTTMAA	AAAAAA

<u>AAAGCCATGAAATTNTAGCCAGCCACTGAATTTGAGTTTTCACTTTGGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCTTTCTTGGTCTT</u> a aaagccatgaaattntagcaagccactgaatttgagttttcactttggtttctaatatgctgtgtgaatcagancagktttcttaccctttcttggtct AAAGCCATGAAATTNTAGCAAGCCACTGAATTTGAGTTTTCACTTTGGTTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCT <u>AAAGCCATGAAATTNTAGCAAGCCACTGAATTTGAGTTTTCACTTTGGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCT</u> AAAGCCATG-AAATTTAGCAAGCCACTGAATTTGAGTTTTCACTTT-GTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCT <u>AAAGCCATGAAATTNTAGCAAGCCACTGAATTTGAGTTTTCACTTTGGTTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCTTTCTTGGTCT</u> 3590 3580 3570 3560 3550 3540 3530 3520 3510 ပေ ф ᇤ

3700 	SACATT	SACATT	SACATT	SACATT	SACATT
3690 	CAATGGCATTA(CAATGGCATTA(CAATGGCATTA	CAATGGCATTA	CAATGGCATTA	CAATGGCATTA
3680	CTATGTATCT CTATGTATCT	CTATGTATCT	CTATGTATCT	CTATGTATCT	CTATGTATCT
3670 I	NTAACATTCCT(NTAACATTCCT(TAACATTCCT	TAACATTCCT	ITAACATTCCT	TAACATTCCT
3660 	ACATATTAR ACATATTAR	ACATATTAR?	ACATATTAR?	ACATATTAR?	ACATATTAR?
3650 	AAATTATTGC AAATTATTGC	AAATTATTGC	AAATTATTGC	AAATTATTGC	AAATTATTGC
3640 	CTATCTCAAA CTATCTCAAA	CTATCTCAAA	CTATCTCAAA	CTATCTCAAA	CTATCTCAAA
3630 	GTWGTAATAC GTWGTAATAC	GTWGTAATAC	GTWGTAATAC	GTWGTAATAC	GTWGTAATAC
3620 	ATAAAATGGG ATAAAATGGG	ATAAAATGGG	ATAAAATGGG	ATAAAATGGG	ATAAAATGGG
3610 	A AATTICCITACIGATAAAAIGGGGIWGIAAIACCIAICICAAAAAITAIIGCACAIAITARAIAACAIICCICIAIGIAICICAAIGGCAITAGACAII B AAITICCITACIGAIAAAAIGGGGIWGIAAIACCIAICICAAAAAITAIIGCACAIAITARAIAACAIICCICIAIGIAICICAAIGGCAITAGAČAIT	C AATTICCTTACTGATAAAATGGGGTWGTAATACCTATCTCAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCATTAGACATT	D AATTICCTTACTGATAAAATGGGGTWGTAATACCTATCTCAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCATTAGACATT	E AATTICCTTACTGATAAAATGGGGTWGTAATACCTATCTCAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCATTAGACATT	F AATTICCTIACTGATAAAATGGGGTWGTAATACCTATCTCAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCATTAGACATT

3710	3720	3730	3740	3750	3760	3770	3780	3790	3800
_	_		_	_	_	_	_		_
A AGGAGAAGCATTITGIGAGGATTIGAAGITGAGAICTTCAICCAAGAAGTAGCITTICAATTIGSTAGAAGCTTAAIGTAGGCAAGCCACTTCATTIT	TTGTGGAGGAT 1	TTGAAGTTGA(SATCTTCATCC	AAGAAGTAG	CITITCAATI	TGSTAGAAGCT	TAATGTAGG	AAGCCACTT	CATTTT
B AGGAGAAGCATTITGIGGAGGATTIGAAGTICAGATCTTCATCCAAGAAGTAGCTTTTCAATTIGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTT	TTGTGGAGGAT 1	TTGAAGTTGA(SATCTTCATCC	AAGAAGTAG	CTTTTCAATT	TGSTAGAAGCT	TAATGTAGG	AAGCCACTT	CATTTT
C AGGAGAAGCATTITGIGGAGGATTIGAAGTICAGATCTICATCCAAGAAGTAGCTTITCAATTIGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTIT	TTGTGGAGGAT 1	TTGAAGTTGA(SATCTTCATCC	AAGAAGTAG	CTTTTCAATT	TGSTAGAAGCT	TAATGTAGG	AAGCCACTT(CATTTT
D AGGAGAAGCATTTTGTGGAGGATTTGAAGTTCATCTTCATCCAAGAAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTT	TGTGGAGGAT1	TTGAAGTTGA(SATCTTCATCC	AAGAAGTAG	CTTTTCAATT	TGSTAGAAGCT	TAATGTAGG	AAGCCACTT(CATTTT
E AGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTT	TGTGGAGGAT 1	TTGAAGTTGA	SATCTTCATCC	AAGAAGTAG	CTTTTCAATT	TGSTAGAAGCT	TAATGTAGG	AAGCCACTT	CATTTT
F AGGAGAAGCATTITGIGGAGGATTIGAAGITGAGATCTTCATCCAAGAAGTAGCTTTTCAATTIGSTAGAAGCTTAATGIAGGCAAGCCACTTCATTTT	TTGTGGAGGAT1	TTGAAGTTGA	SATCTTCATCC	AAGAAGTAG	CTTTTCAATT	TGSTAGAAGCT	TAATGTAGGC	:AAGCCACTT	CATTTT

CAGAACTTGTTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGTCAGAGAGGAGGGGTGCCTTAAAAATGTTGTGGGCCAAGCCACATGAGATCAAAGA CAGAACTTGTTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGTCAGAGAGGGTGCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGA

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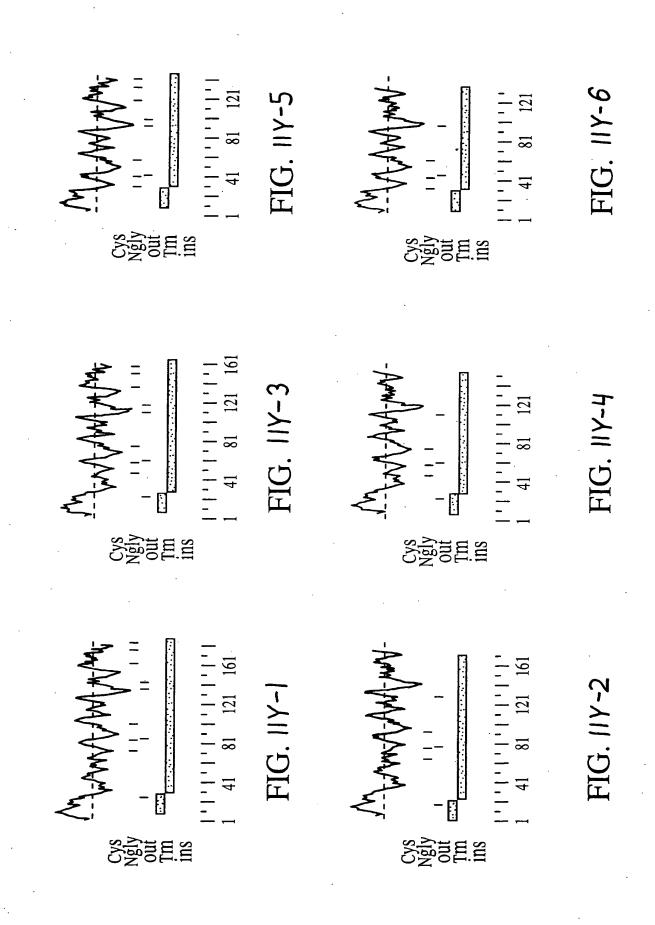
CAGAACTIGTTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGTCAGAGAAGGGGTGCCTTAAAAATGTTGTGGGCCAAGCCACATGAGATCAAAGA CAGAACTIGITITACICATITATAATATGGGAATAAAATTTGTGCAAGTCAGAGAAGGGGTGCCTTAAAAATGTTGTGGGCCAAGCCACATGAGATCAAAGA

CAGAACTTGTTTACTCATTTATAATATGGGAATAAAATTTGTGCAAGTCAGAGAAGGGGTGCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGA

noysoment to the second

4000	SCCA	SCCA	SCCA	SCCA	SCCA
7	CAGAC	CAGA	CAGA	CAGAC	CAGAC
3990	A CACACTITICATGACCTCAAATGIGGGCCCAGCCTAGGICAGCCAACCCCCAICCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCA B CACACTITICATGACCTCAAATGIGGGCCCAGCCTAGGICAACCCCCATCCAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCA	C CACACTITICATGACCTCAAATGTGGGCCCCAGCCTAGGTCAGCCCCATCCCAACCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCA	D CACACTITICATGACCICAAAIGIGGGCCCAGCCIAGGICAGCCAACCCCCAICCAACCTIAGACTCACGAACAAAICCACCIGAGAICAGCAGAGCCA	E CACACITITCATGACCICAAATGTGGGCCCAGCCTAGGTCAGCCAACCCCCATCCAACCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCA	F CACACTITICATGACCICAAAIGIGGGCCCAGCCIAGGICAGCCCAACCCCCAICCAACCCTIAGACICACGAACAAAICCACCIGAGAICAGCAGAGCCA
m	CTGAG	CTGAG	CTGAG	CTGAG	CTGAG
3980	rccac rccac	rccac	rccac	rccac	rccac
œ.	ACAAA?	CAAA	CAAA	CAAA.	ACAAA!
3970 	ACGA/	ACGA	ACGA	ACGA	ACGA?
39	GACTC	GACTC	GACTC	GACTC	GACTC
09 —	CCTTA	CCTTA	CCTTA	CCTTA	CCTTA
3960 	CAAC	CAAC	CAAC	CAAC	CAAC
o –	CCATC	CCAT	CCAT	CCAT	CCAT
3950 	AACCC	AACCC	AACCC	AACCC	AACCC
0 –	CAGCC	cagcc	CAGCC	CAGCC	CAGCC
3940	PAGGT	raggr	PAGGT	PAGGT	raggi
	AGCC1	AGCC	'AGCC1	'AGCC	'AGCC1
3930	22255	2225	22255	ರಿಯಾ	ວວວອອ
	ATGTG	ATGTG	ATGTG	ATGTG	ATGTG
3920 	TCAA	TCAA	TCAA	TCAA	TCAA
	TGACC	TGACC	TGACC	TGACC	TGACC
3910 	TTTCA	TTTCA	TTTCA	TTTCA	TTTCA
	ACACT'	CACT	CACT	\CACT	ACACT
	A CF B CA	CC	D C	E CA	F CF

Fig. 11X-14



First of the contraction of the

60 120 180 230	278	326	374	422	470
GCGTCCGGTT TGCTTGGAGA TGCTGCTAAA ACAGAGAGC TGTGAACAAG AGCAGGAGCA TACATTCAGA AGACAAGGAG CCCTGCTCGC TGCACCGAAT AAAGACTCCT ATCTGTATGC CAACCCAGAC TTCCAGAAAG AGATCAGATC	ATC AAA GTT GTT GGA ATG ACC TTT TTT CTG CTG TAT TTC Ile Lys Val Val Gly Met Thr Phe Phe Leu Leu Tyr Phe 15	TTT GGC AAA AGT AAT GAT GGC TTC GTC CCC ACG GAG AGC Phe Gly Lys Ser Asn Asp Gly Phe Val Pro Thr Glu Ser 35	ACT AGT GTG CAG AAT GTC TCA CAG ATC TTT GGG AGA AAT 37 Thr Ser Val Gln Asn Val Ser Gln Ile Phe Gly Arg Asn 50	ACC ATG CCT ACA AGG AGC TAT GGA ACA GTC TGT CCC AGA Thr Met Pro Thr Arg Ser Tyr Gly Thr Val Cys Pro Arg 65	TTT CAC CAA GGA AAA TGC TTT TTC TTC TCC TTC TCC GAA Phe His Gln Gly Lys Cys Phe Phe Phe Ser Phe Ser Glu 80
CCCAC TACCG ATCAA ATCCC	GTA GTG Val Val	CAG GTT Gln Val	GGA ACC Gly Thr 45	GAA AGT Glu Ser	TGG GAT Trp Asp
GTCGACCCAC GACATTACCG ATCTTATCAA CCTGAATCCC	GTA G1 Val Va	CCA C2 Pro G1	TAC GC Tyr GJ	GAC GA Asp G] 60	AAC TC Asn Tı

Fig. 11Z-1

518	566	614	662	710	758
ACA Thr	ATA Ile	GAG Glu	ACC Thr 155	ACA Thr	ATG Met
TCC	GAC Asp	GGA Gly	GTT Val	AAG Lys 170	GAA Glu
GGA Gly 105	CAG Gln	CCT Pro	AAT Asn	ACG Thr	TGC Cys 185
CAA Gln	CTT Leu 120	CAG Gln	GGC	CTG Leu	ATC Ile
ACA Thr	TAT Tyr	CGT Arg 135	AAT Asn	GGT Gly	TGG Trp
GCA Ala	AAG Lys	GTA Val	TTC Phe 150	ATA Ile	CGC Arg
TGT Cys	CTG Leu	TTG Leu	GTG Val	ACT Thr 165	\mathtt{TAT}
TAT Tyr 100	AAA Lys	GGT	TCT Ser	GTC Val	AGC Ser 180
GAT Asp	GAG Glu 115	ATT Ile	AAC Asn	TGT Cys	GTC Val
ATG Met	CCA Pro	TTT Phe 130	AAC Asn	GAC Asp	GAA Glu
AGC Ser	ACT Thr	TAC Tyr	ATC Ile 145	TTC Phe	TGT Cys
GAC Asp	AAC Asn	AAT Asn	TGG Trp	AAC Asn 160	TCA Ser
AAA Lys 95	GTC Val	GAG Glu	CGC Arg	CAG Gln	GCA Ala 175
TGG Trp	ATT Ile 110	ATT Ile	TGG Trp	GAC Asp	GCT Ala
CCT	GCA Ala	GGT Gly 125	AAG Lys	CAG Gln	GAT Asp
TCA	CIG	GCT Ala	AAA Lys 140	AAT Asn	TAT Tyr

Fig. 11Z-2

<u>odysolicianaca</u>

AAT GCC AAA Asn Ala Lys	TGATCATAG	AAT GCC AAA TGATCATAGA TCTCTACAAG AGTGAATTTT Asn Ala Lys	AGTGAATTT	: TACAGAGCTA	~	807
190						
SCAAAGGAGA	TTAGTTGTGA	CTGAAACCAG	CCCAGGAAAT	ATAGAGCATC	AAAGACTGTG	867
CCCATCTTCC	ATAGGTGGAG	TTCCCTATTG	AATCCTCAAA	GTCAATTTGT	TACTCCACAA	927
ACATCTTCAC	ATAGTAAAAC	TCCCTTTCTG	ACCAAGTATT	CCCTAAGACC	ACACTTCCTG	987
TGAGAGGGGA	CTGGATTCTA	GTTATCTGCA	GACAGAGCCA	GGATTCTGGA	GATGAAATCA	1047
ATATGGAAAT	GCAGTCTGTT	TCTGTAGAGC	TGAGCCTTTT	AACTAATCAG	TAGGGTTTTG	1107
ICTGTTGTCA	GAACTGTTTG	ATCCTTAGAG	AACATGCCCA	CGCCACTGAG	GAGAAACTGC	1167
ICGTGGAACA	GATATGAGAA	CTGTTAGGAA	GCACTATGGG	CAGAAGAATA	TAAACTTGGC	1227
ITCACAACAT	CCCCCATTCC	AGAAAGCCTC	CCATTCCCAT	ACAACATCGT	AGAAGCAGAG	1287
STCCTTCTGA	ATTGGGGAAG	GACCICTACA	GCTCGACTTG	GTACTGAACA	AATATTGAGG	1347
SAATGAAGAA	AGTTCTGAAT	AGGACAGAGA	TAAACAAGGA	GGAGAAGGAA	AGAGATAGGA	1407
AGAAAGGAGA	AGTGGGAAGG	AGGGGGAAAA	GGAATGATGG	GCAGGAGAAA	AAGAGACAGG	1467
AGCAGCCAGG	AAAAACACTC	AAGCTAAATT	TTTTTCAGGT	TTTGGATAAA	ATCTATTGTG	1527
ACATAAATAA	TATCTTTTCA	TTAGAAGAGA	AAAGGCAAAA	TTGGGGACAA	ATGGGCACCA	1587
TGAGAGATGA	AGCAGAGGTT	AATTTGATCA	CAAGGAAAGA	AAGGCAGGAA	TGAGGTTGAA	1647
AACTTTTGG	ATACCTTGGC	TGTTATCTCA	AGAAGGTACA	AGCTGCATAA	AGTATAGGAG	1707
AAAAGAGATG	TGCTGGTTGT	TTTAAGTAGC	AAAATTAAA	CTACAGAGAA	GCCTATAGAA	1767
AGCTAAAGGA	ATTAAAACCA	TCCAATAATC	AATTCATTAT	TTTCAACTAA	TAGCAATATG	1827
TATGTGCATT	ACTAGTCAAA	ATAAATTGTG	AATTCTGTTA	TTATAAAAA	AAAAAAAG	1887
೨೨೨೨೨೨೨೨						1896

Fig. 11Z-3

rogen of the

MI289	•	09
HI289	ATGAACTGGCACATGATCATCTCGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATG	09
MI289	ACCTITITICIGCIGIAITICCCACAGGIITITIGGCAAAAGIAAIGAIGGCITCGICCC	120
HI289		120
MI289	ACGGAACCACTAGTGTGCAGAATGTCTCACAGATCTTTGGGAGAAATGAC	180
H7289		171
707111		۲ -
MI289	GAAAGTACCATGCCTACAAGGAGCTATGGAACAGTCTGTCCCAGAAACTGGGATTTTCAC	240
HI289	AACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCAAAGACTGGGGAATTTTAT	234
MI289	CAAGGAAAATGCTTTTTCTCCTTCTCCGAATCACCTTGGAAAGACAGCATGGATTAT	300
HI289	CAAGCAAGATGTTTTTTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTT	294

MI289	ATGAACTGGC	09
HI289	AIGAACIGGCACAIGAICAICICIGGGCIIAIIGI II IIIIII I IIIIIIIIII	09
MI289	ACCITITITICICCIGIATITICCCACAGGITITITIGGCAAAAGIAAIGAIGGCITCGICCCC	120
HI289	ACCITATITCTACTITATITCCCACAGATITITAACAAAAGTAACGAIGGITICACCACC	120
MI289	ACGGAGAGCTACGGAACCACTAGTGTGCAGAATGTCTCACAGATCTTTGGGAGAAATGAC	180
HI289	ACCAGGAGCTATGGAACAGTCTCACAGATTTTTGGGAGCAGTTCCCCAAGTCCC	174
MI289	GAAAGTACCA	240
HI289	AACGGCTTCATTACCACAAGGAGCTATGGAACAGTCTGCCCCAAAGACTGGGAATTTTAT	234
MI289	CAAGGAAAATGCTTTTTCTCTCCTTCTCCGAATCACCTTGGAAAGACAGCATGGATTAT	300
HI289	CAAGCAAGATGTTTTTTTTTCTTATCCACTTCTGAATCATCTTGGAATGAAAGCAGGGACTTT	294

FORFER OF CA. FORE

MI289	TGTGCAACACACAGGATCCACACTGGCAATTGTCAACACTCCAGAGAAACTGAAGTATCTT	360
HI289		354
0		(
MIZ89	CAGGACATAGCT'GGTATT'GAGAATTTACTTTTATT'GGT'TTGGT'ACGT'CAGCCT'GGAGAAA 	420
HI289	CAGGACATAACTGATGCTGAGAAGTATTTTATTGGCTTAATTTTACCATCGTGAAGAAAA	414
MI289	AAGTGGCGCTGGATCAACACTCTGTGTTCAATGGCAATGTTACCAATCAGGACCAGAAC	480
HTORG		7 7 7
70711		r ~
MI289	TTCGACTGTGTCACTATAGGTCTGACGAAGACATATGATGCTGCATCATGTGAAGTCAGC	540
HI289	CAGAATTTCAACTGTGCGACCATTGGCCTAACAAAGACATTTGATGCTGGTGACATCAGC	534
MI289	ratcgctggatc	
HI289	TACCGCAGGATCTGTGAGAAGAATGCCAAA 564	

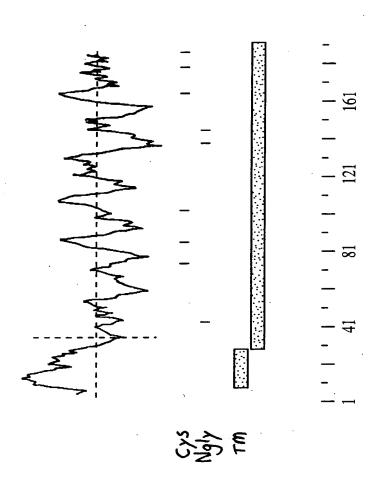


FIG. 112-6

DOFFOIRO OF TEOR

19 58 39 59 178 79 99 119 358 139 418 159 478 S TCC V GTG GGG T ACG GGA Y TAT W TGG G Q CAG E D GAT S TCC T ACG I ATC F GGA CCT TGG Y TAT A GCT ာ TGC I ATC D GAT L TTA 3 ATG \mathbf{z} TTC I ATC A GCT R AGG F R AGA Y TAC GIC > AAC K AAA T ACC I ATC I ATC $_{\rm TGT}^{\rm C}$ L Z T ACT GAA C TGC M ATG C TGC I ATC I ATC A GCT ഥ GIC \gt $_{
m L}$ Q CAG GGA A GCC TTTK AAA E GAA GCT GTT M ATG M ATG GGA N AAT GGA A GCT \triangleright GTG GIG T ACG R AGG R AGA G 360 A GCC LCIT ACA ATC I ATC A GCC L E GAG L V GTT \vdash 299 ധ AAC N AAC A GCA I ATC L W TGG R CGT z GIG AAC A GCT Q CAG A GCC I ATT S AGC K AAA z M ATG GAA H CAC V GTG Q CAG M ATG Q CAA L CTA ഥ GGA M ATG I ATT R AGG D GAC A GCT PCCT A GCC GTT V GTG \mathbf{F} P F ITC K AAG IATC V GTT GGT ᠐ A GCC C TGC V GTG L s ICT A GCT N AAT GGT TCG K AAG V GTG $_{
m ITG}$ V GTG N AAT LCTT ഗ L GTG E GAG V GTG M ATG A GCT F TTTഥ AGA W TGG $_{
m L}$ S TCC M ATG S TCA N AAT 24 $_{
m L}$ W TGG D GAC L $_{\rm CTG}$ M ATG 9 9 N AAC ഗ

Fig. 12A

	LI E	> 8	ΠĘ	H	> [ტ წ	ს წ	Ø 0	ьÉ	ر ت (ည (E	ပ ပ	> [FH E	ပ E	ပ (Z 6	179
ACC ACG GCA CTG GTG CTG ATT GTT GGA GGA GCT CTG TTC TGC TGC GTT TTT TGT TGC AAC	GTG O	O	J.T.G	ATT	GTT	GGA	GGA	GCT	CTG	TIC	IGC	IGC	GTT	$_{ m TTT}$	$_{ m TGT}$	TGC	AAC	538
လ လ	ഗ		×	ĸ	×	ഗ	Н	Д	ഗ	н	~	₽	EH	Ø	×	ഗ	×	199
SAA AAG AGC AGT AGC TAC AGA TAC TCG ATA CCT TCC CAT CGC ACA ACC CAA AAA AGT TAT	AGC		rac	AGA	TAC	TCG	ATA	CCT	ICC	CAT	၁၅၁	ACA	ACC	CAA	AAA	AGT	TAT	598
K	×		ഗ	വ	ഗ	\triangleright	⊁	လ	ഷ	ഗ	Q	≯	Λ	*				215
CAC ACC GGA AAG AAG TCA CCG AGC GTC TAC TCC AGA AGT CAG TAT GTG TAG	AAG		TCA	SCG	AGC	GIC	TAC	ICC	AGA	AGT	CAG	TAT	GTG	TAG				649
ITGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATGACAAAAATTTATTT	TAAC CTGI	: : : '	TTAC PCTTA	TATA VACTG	AAGC ;CCTA	CATG	CAAA TAAT	TGAC	CAAA? \GGA?	AATCI \CTGI	ratai GCAI	rtaci rcago	TTTCI	rcaa <i>i</i> rtato	AATGO SATTO	SACC(CTATA	SCAA	728
<pre>PATTTCAGCAGAATGAGATATTAAACCCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTTGTTTTCTAAGGTGGTTTC</pre>	AGAT		ATTAE	AACCC	:AATG	CTTT	GATT	GTTC	TAGE	AAAGI	TATAG	STAAT	[TTG]	rttT(CTAAC	3GTG(STTC	988
AAGCATCTACTCTTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTTCTCCAC	TTATC	()	ATT	PACTI	CAAA	ATGA	CATI	GCTA	AAAG2	ACTGC	ATT	\TTT	ract?	ACTG1	FAAT 1	rtct(CCAC	965
SACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCACATAGAGACATGCTTATATATGTTTTATAAAATG	ACATA	\sim	GATG	SAGTG	TAAC	ATTT	ATAT	CTC	1CAT	4GAG2	ACATO	3CTT?	ATAT(3GTT1	FTAT	LTAA!	AATG	1044
AAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGT	ACACT		GAA1	TAAAT	AGAA	CTCA	ACTA	TTGC	TTTT	rcage	3GAAZ	4TCA1	rgga1	ragg	3TTG	AAGAA	4GGT	1123
<pre>PACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAAAATGAAGGCTTTAATCAG</pre>	AAAAA	\sim	CAGC	TTAG	GGAT	TAAT	GTCC	TCCF	TTTF	TAAI	GAAG	3ATT?	AAAA ?	rgaa(3GCT1	LTAA	rcag	1202
CATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTC	TGAAT	-	GGCI	TTCI	GATA	TGCT	GTTI	TTT	1GCC1	LAGG2	AGTT?	4GAA2	ATCCI	[AAC]	FTCT	TTAT(CTC	1281
ITCTCCCAGAGGCTTTTTTTTTTTGTGTATTAAATTAACATTTTAAAAAGCAGATATTTTGTCAAGGGGCTTTGCAT	TTTT		TTC1	TGTG	TAT	AAAT	TAAC	ATTI	rtta?	1AAAG	3CAG2	TAT	rttg:	rcaa(3666(CTTT(SCAT	1360
ICAAACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAGTGTGTGATCTAAGAAAAGTGATGGTTTTAGGAAAGTG	AGGGC	7)	TAT	ACTCA	GAAG	AAAG	ATA	AAAGI	rgrg2	ATCT?	AAGA.	AAAA(STGA	rggrı	rtta(GGAAI	AGTG	1439
AAAATATTTTTTTTTTTTTTTTGAAGAAGAATGATGCATTTTTGACAAGAAATCATATATGTATG	TIGTA	4	TTT	SAAGA	AGAA	TGAT	GCAI	TTTG	3ACA?	4GAA?	TCA1	LATA 1	'GTA'	rgga1	LATA 1	TTT1	AATA	1518
AGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAA	ACTTT($\stackrel{\sim}{\vdash}$	3AGC	FTTT	ATCA	ATAT	AAAT	AAAZ	4GAG(CAGAZ	\AAA1	ratg:	rctt(3GTT]	rtca1	rttg(CTTA	1597

Fig. 121

CCAAAAAAACAACAACAAAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCA	16
TTTTTGTTCTGTGAAAAATAAATTTCCTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTT	17
TCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCT	18
GTTCTATTTGCTTTATACATTTATATTAATTAATTGTACATTTTTTTT	19

Fig. 12C

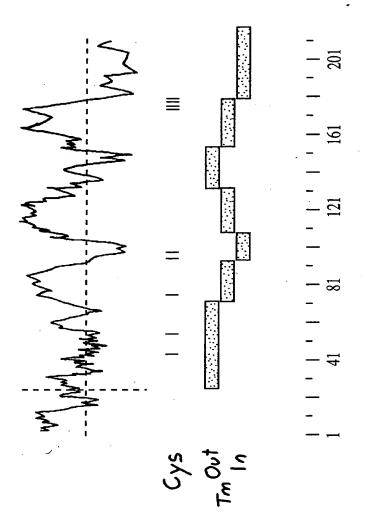


FIG. 12D

DKFZ I309	G	(TGGAATGGT	-GGGCA :::: TGGGCACAGTG 30		 STCATGCCTC? 50	 AGTGGAGAGTGTC 7	 CG 70
DKF2 I309			 TTTGAAAACT	 TCTGGGAAGG	 SACTGTGGATG	SAATTGCGTGAGGC	, vc
DKFZ		 	 				> ,
1309	AGGCTAACATCAGGATGC 150	CAGTGCAAAA 160	TCTATGATTC 170	CCTGCTGGC1 180	CTTTCTCCGC 190	GATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGC 100 160 170 180 190 200 210	ಬ ಂ
DKFZ							ı
1309	CAGAGGACTGATGTGTG 220	CTGCTTCCGT 230	GATGTCCTTC 240	TTGGCTTTC? 250	TGATGGCCAT 260	rccttggcatgaaa 270 280	& 0
DKFZ							
1309	TGCACCAGGTGCACGGGGGCAAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCA 330 340 350	GGACAATGAG 300	AAGGTGAAGG 310	CTCACATTCI 320	:GCTGACGGC1 330	IGGAATCATCTTCA 340	A 0

Fig. 12E

DKFZ		 	 - - - - -	1 1 1 1 1 1			
1309	I309 TCATCACGGGCATGGTG	GTGCTCATCC 370	CCTGTGAGCTG 380	GGTTGCCAA. 390	IGCCATCATC 400	TGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAA 370 380 390 400 410 420	TAA 420
DKFZ							!
1309	CTCAATAGTGAA 430	CCCAAAAACC 440	STGAGCTTGGA 450	GAAGCTCTCT 460	TACTTAGGAT 470	TGTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTG 440 450 460 470 480 490	CTG 490
DKFZ		 					}
1309	GTGCTGATTGTT 500	AGCTCTGTTC 510	CTGCTGCGTTT 520	TTTGTTGCA1 530	acgaaaagag 540	GGAGGAGCTCTGTTCTGCTTTTTTTTTTGTTGCAACGAAAGAGCAGTAGCTACAGAT 510 520 530 540 550	GAT 560
DKFZ				 	; 		1
1309	ACTCGATACCTT 570	CGCACAACCC 580	CAAAAAAGTTA 590	.TCACACCGG/ 600	AAAGAAGTCA 610	CCCATCGCACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTC 580 590 600 600 610	CTC 630
DKFZ						 	1
I309	I309 CAGAAGTCAGTATGTGT 640	AGTTGTGTA1 650	rgttttttaa 660	CTTTACTATA 670	AAAGCCATGC 680	TGTGTAGTTGTGTTTTTTTTAACTTTACTATAAAGCCATGCAAATGACAAAATC 650 660 670 670 680 690	ATC 700

Fig. 12F

	₫ ○	()()		
	ATTA 770	ATGC :::: ATGC 840	ATTT :::: ATTT 910	ATGT :::: ATGT 980
	TTA	CCCA	TATC	ATT::::XATT
	AATC 0	20 AAAC :::: AAAC 0	90 TTTT::::TTTT	160 ATAGC ::::: ATAGC
	CCTA 760	2 ATTA :::: ATTA 830	CICTI	16 ACAT::::ACAT:
!	ACTG	AGAT :::: AGAT	CTAC ::::	CACG
	TTAZ 0	10 20 GAA T GAGATATTAAACCCAATGC ::::::::::::::::::::::::::::::::::::	80 CAT(::: CAT(150 TCTC :::: TCTC
İ	STTCT 750	1 GAA' ::: SAGAA' 820	8 CAAGC ::::: CAAGC 890	15(ATTTC: ::::: ATTTC: 960
	ACT(GTT(::::	GTAZ :::: GTAZ
	CAAAATGGACCCCAAAGAAACTTTGATTTACTGTTCTTAACTGCCTAATCTTAATTA 720 730 740 750 760 770	10 20	50 80 90 GAAAGTATAGTATTTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTT ::::::::::::::::::	120 140 150 160 ATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGT ::::::::::::::::::::::::::::::::
.	TTG2 7	 GCT2	TAA(::::	TACT:::
	AACT	 \TAA		\TTT :::: \TTT
.	AAGA. 730	 TTCT?	60 TTGT1 :::: TTGT1	130 CATTA::: CATTA:
	CAA 7	 GAT 8	AATT SERVE	00 I C C C C C C C C C C C C C C C C C C
	ACCC	 TTAT	AGT <i>P</i> :::: AGT <i>P</i>	AGAC :::: AGAC
	ATGG	 CTAT	50 GTAT: :::: GTAT: 860	120 CTAA :::: CTAA 930
	AAAA	CAGC	AAAC :::: AAAC 8	TTGC :::: TTGC
				SACA:
	CTTT 710	.TGTG	40 GTTC: :::: GTTC: 850	110 ACTTCAAAATGAC ::::::::::: ACTTCAAAATGAC 920
	TTA	AAC	ATT ::: ATT	CAA ::: CAA
	TATATTACTITCT 710	 CAGGAACTGTGCA 780	30 40 TTTGATTGTTCTA ::::::::::: TTTGATTGTTCTA 850	0. 110 ACTTCAAAATGAC :::::::::: ACTTCAAAATGAC 920
DKFZ -	I309	DKFZ -	30 40 DKFZ TTTGATTGTTCTA ::::::::::::::::::::::::::::::::::	100 DKFZ ACTTCAAAATGAC ::::::::::::::::::::::::::::::::::::
DK	I3	DK I3	DK I3	D K

Fig. 12G

TGAAATGC ::::::: TGAAATGC 1050	TTGAAGAA ::::::: TTGAAGAA 1120	TAAAATGA ::::::: TAAAATGA	GGAGTTAG :::::: GGAGTTAG
230 TATTTAAAA' :::::::: TATTTAAAA' 1040	300 .rggaraggg' ::::::::::::::::::::::::::::::::::	370 AATGAAGAT' :::::::: AATGAAGAT' 1180	440 TTTAGCCTA(::::::TTTAGCCTA()
220 TATATGGTTT ::::::::: TATATGGTTT 1030	290 AGGGAAATCA :::::::: AGGGAAATCA 1100	360 CTCCATTTAT :::::::: CTCCATTTAT	430 TATGCTGTTT ::::::::: TATGCTGTTT 1240
210 SAGACATGCT' :::::::: SAGACATGCT' 1020	280 ATTGCTTTTC:::::	350 SATTAATGTC: ::::::::: SATTAATGTC	420 3GCTTTCTGA ::::::::: 3GCTTTCTGA 1230
190 200 210 220 230 TAACATTTATATCTCACATAGACATGCTTATATGGTTTTTAAAATGAAATGC ::::::::::::::::::::::::::::::::::::	0 250 260 270 280 290 300 CAGTCCATTACACTGAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAA :::::::::::::::::::::	320 330 340 350 360 370 SGTTACTATTAATGTTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAAATGA :::::::::::::::::	400 410 420 430 440 CATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAG :::::::::::::::::::::::::::::
190 'AACATTTAT? :::::::::	260 GAATAAATAC ::::::::::::::::::::::::::::::	330 :GTTTTAAAAA :::: :::::::::::::::::::::::::	400 ATTGTAAAGC::::::::::::::::::::::::::::::
170 180 DKFZ ACATAGATGAGTG1 :::::::::::::::::::::::::::::::::::	240 250 DKFZ CAGTCCATTACACT ::::::::::::::::::::::::::::	320 DKFZ GGTTACTATTAATT :::::::::::::::::::::::::::	380 390 DKFZ AGGCTTTAATCAGC :::::::::::::::::::::::::::::::::::
170 DKFZ ACAT :::: I309 ACAT	240 DKFZ CAGT :::: I309 CAGT	310 DKFZ GGTT :::: I309 GGTT	380 DKFZ AGGC :::: I309 AGGC

Fig. 12H

470 480 490 500 510 :TITATCCTCTTCTCCCAGAGGCTTTTTTTTTTTTTTTAATTAA	540 580 TGTCAAGGGGCTTTGCATTCAAACTGCTTTTCCAGGGCTATACTCAGAAGAAAGA	590 600 610 620 630 640 650 DKFZ AAAGTGTGATCTAAGAAAAGTGATGTTTTAGGAAAGTGAAAATATTTTTTT	660 680 690 710 720 DKFZ AATGATGCATTTTGACAAGAATCATATATATGTATGTATTTTAATAAGTATTTGAGTACATTGACTTTG ::::::::::::::::::::::::::::::::::::
510 TTAAATTAA :::::::: TTAAATTAA	580 ATACTCAGA :::::::: ATACTCAGA 1390	650 TTTTTGTAT ::::::::: TTTTTGTAT	720 'ATTTGAGTA' :::::::::
500 TTCTTGTGTA ::::::::: TTCTTGTGTA 1310	570 TTCCAGGGCT :::::::: TTCCAGGGCT	640 AATATTTTG :::::::: AATATTTTTG	710 TTTAATAAGT ::::::::: TTTAATAAGT
490 GGCTTTTTTT :::::::: GGCTTTTTTTT	560 CAAACTGCTT :::::::: CAAACTGCTT	630 GGAAAGTGAA :::::::: GGAAAGTGAA	700 ATGGATATAT ::::::::: ATGGATATAT 1510
470 480 490 500 510 TTATCCTCTTCTCCCAGAGGCTTTTTTTTTTTTTAATTAA	540 580 TGTCAAGGGGCTTTGCATTCAAACTGCTTTTCCAGGGCTATACTCAGAAGAAAGA	620 GATGGTTTTA ::::::::: GATGGTTTTA	680 690 700 710 720 GACAAGAAATCATATATGGATATATTTTAATAAGTATTTGAGTACAGACTTT::::::::::
470 CTTTATCCTC ::::::::: CTTTATCCTC		610 AAGAAAAAGT ::::::::: AAGAAAAAGT 1420	680 TGACAAGAAA ::::::::: TGACAAGAAA
450 460 DKFZ AAATCCTAACTTC ::::::::::::::::::::::::::	520 530 DKFZ AAAGCAGATATTT :::::::::::::::::::::::::::::::	590 600 610 620 630 640 650 DKFZ AAAGTGTGTTTTTGGAAAGTGAAAGTGAAATATTTTTTTT	660 670 DKFZ AATGATGCATTTT :::::::::::::::::::::::::::::::::
450 DKFZ AA :: I309 AA 1260	520 DKFZ AA :: I309 AA 1330	590 DKFZ AA :: 1309 AA	660 DKFZ AA :: I309 AA 1470

Fig. 12I

AAAACAA :::::: AAAACAA	GTCATTT :::::: GTCATTT	AATACTG :::::: AATACTG	TCTGTCT::::TCTGTCT
790 SCTTACCAAA ::::::::: SCTTACCAAA	860 AGTCAAAATT :::::::: AGTCAAAATT 1670	930 AAAATCTGTA ::::::::: AAAATCTGTA 1740	1000 rgrgrcgAcG ::::::::: rgrgrcgAcG
730 740 750 760 770 780 790 DKFZ AGGTTTCATCAATATAAATAAGAGCAGAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAACAA ::::::::::::::::::::::::	800 810 820 830 840 850 860 DKFZ CAACAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTT :::::::::::::::::::::::::::::::::	870 880 900 910 920 930 DKFZ TTGTTCTGTGAAAATTTCCTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTG ::::::::::::::::::::::::::::::::::::	940 950 1000 DKFZ TATTTTCTGTTTATTCCAAATTTGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCT
770 ATATGTCTTG(:::::::: ATATGTCTTG(1580	840 rgcrccrarg:::: rgcrccrarg:	910 CATTTCTGTT::::::::::::::::::::::::::::::	980 SACAATCCAA: ::::::::
760 3AGCAGAAAA :::::::: 3AGCAGAAAA 1570	830 ;AACTTCACC1 ::::::::	900 TTCTTGTACC::::::::::::::::::::::::::::::	970 ::::::::::::::::::::::::::::::::::::
750 .TAAATAAAAG .::::::::: .TAAATAAAAG	820 GTCCTTTGAG :::::::::	890 ATAAATTTCC ::::::::: ATAAATTTCC 1700	960 TTCCAAATTT ::::::::::::::::::::::::::::
0 AGGTTTCATCAATA :::::::::::: AGGTTTCATCAATA 0	810 AAAAAAGTT :::::::: AAAAAAGTT	0 TTGTTCTGTGAAAA :::::::::::: TTGTTCTGTGAAAA	0 TATTTTTCTGTTTA ::::::::::: TATTTTTCTGTTTA 0
730 DKFZ AGGT :::: 1309 AGGT	800 DKFZ CAAC :::: I309 CAAC 1610	870 DKFZ TTGT :::: 1309 TTGT 1680	940 DKFZ TATT :::: I309 TATT 1750

Fig. 12J

nayana an <u>natana</u>

1010	0	1020	1030	1040	1050	1060	1070
DKFZ	AGCTT	AAATGAATGTG	TTCTATTTGCT	TTATACATTT	ATATTAATA	AATTGTACAT'	DKFZ AGCTTAAATGAATGTGTTCTATTTGCTTTTATATTATTAATAAATTGTACATTTTTCCAAAAAAA
	••	•••		•••	•••	•••	
I309	AGCTT	AAATGAATGTG	TTCTATTTGCT	TTATACATTT	ATATTAATA	AATTGTACAT	I309 AGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTTCTAAAAAAA
1820	0	1830	1840	1850	1860	1870	1880
1080	0	1090					
DKFZ	AAAAA	DKFZ AAAAAAAAAA					
	••	•••					
1309	AAAAA	I309 AAAAAAAAAAAAAAAAA	AAAA				
1890	0	1900					

Fig. 12K

	60 70 80 90 100 110 CTCAGTGGAGAGTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACTTCTG :::::::::::::::::::::::::::::::::	130 140 150 160 170 180 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTG :::::::::::::::::::::::::::::::	200 210 220 230 240 250 CGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTTCCGTGATGTCCTTCTTGG::::::::::
GCTGTTT . ATGGCAACCTACGCTCTTCAAATGGCTGCACTGGTG 10 20 30	50 60 70 I309 TCACTGTCATGCCTCAGTGGAGAGTGTCGGCCTTCA : :::::::::::::::::::::::::::::::::::	120 130 150 150 150 150 160 170 180 I309 GGAAGGATGAATTGCGTGAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTG ::::::::::::::::::::::::::::::::	190 200 210 220 230 240 250 250 240 250 CTGGCTCTTTCTCCGGACCTACAGGCCAGCCAGAGGACTGATGTGTGCTTCCGTGATGTCCTTCTTGG::::::::::
I309 CLAUD8	I309 CLAUD8	I309 CLAUD8	I309 CLAUD8

Fig. 12I

<u>naysatan attant</u>

320 GCTCA :. 1GCCG 350	390 36GTT :::: 3GGTT 420	460 GGAGAAG :::::: GGAGAAG 490	530 TTTTG ::::: TTTTG 560
270 280 290 300 310 CCATCCTTGGCATGAAATGCACCAGGGGGGACAATGAGAAGGTGAAGGGGGGCACAATGAGAAGGTGAAGGGGGGGG	380 CCCTGTGAGCTGGGT :::::::::: CCCTGTCAGCTGGGT 410	450 CGTGAGCTTGGA :::::::: CGCGAGCTGGGA	480 490 500 510 530 GATGGACCACGGCACTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTG :::::::::::::::
300 GGGGGACAATG :::::::::: GGGGGACGATG 330	370 380 GTGGTGCTCATCCCTGTG :: :::::::::: GTTGTGCTCATCCCTGTC 400 410	430 440 450 TAGTGAATGTTGCCCAAAAACGTGAGCTT :::::::::::::::::::::::::::::::::::	480 490 500 510 520 TGGACCACGGCACTGGTGCTGATTGTTGGAĞGAGCTCTGTTCTGCTGC ::::::::::::::::::::::::
290 accaggTgcac ::::::::: accagaTgcac 320	340 350 360 SGCTGGAATCATCTTCATCACGGGCATGGT .::::::::::::::::::::::::::::::::::::	430 AATAGTGAATG : ::::::: ACTGGTGGATG	500 CTGATTGTTGG ::::::::: CTGATCGCTGG
280 CATGAAATGC :::::::: AATGAAGTGC 310	350 ATCTTCATCA :::::::: ATCTTCTTCA 380	420 TTCTATAACTCAA :::::::::: TTCTACAACCCAC 450	490 GGCACTGGTG .::::::: AGCGCTGGTG
270 ccarccrrgg :::::::: ccarccrcgg	340 GGCTGGAATC ::::::: AGCCGGAATC 370	410 ATCAGAGATT' ::::::::: ATCAGAGACT' 440	480 GATGGACCAC : :::::: GCTGGACCAC
260 270 320 320 300 300 310 320 I309 CTTTCATGATGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCA :::::::::::::::::::::::::::::::::::	330 340 350 360 370 390 390 I309 CATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTT :::::::::::::::::::::::::::::::	400 410 420 430 440 450 460 I309 GCCAATCATCATCATAACTCAATAGTGAATGTTGCCCCAAAAACGTGAGCTTGGAGAAG ::::::::::::::::::::::::::::::	470 CTCTCTACTTAG : :::::::: CCCTCTACATAG 500
I309 CLAUD8	I309 CLAUD8	I309 CLAUD8	I309 CLAUD8

Fig. 12M

norequentation

(540	550	560	570	580	590	009
I309 CLAUD8	TTGCAACGAAAA(:::::::::::::::::::::::::::::	SCAGTAGCTAC :::. ::: SCAACAGTTAC 580	AGATACTCGA1 ::.:::::: AGGTACTCGG1 590	ACCTTCCCA ::::::: ACCATCCCA 600		SAGCAGTAGCTACAGATACTCGATACCTTCCCATCGCACAACCCAAAAAGTTAT :::::. :: ::::::::::::::::::::::::::::	rcac ::: ccac 630
I309 CLAUD8	610 ACCGGAAAGAAGT .::::::::: GCCGAAAGAGAT 640	620 630 640 CACCGAGCGTCTACTCCAGAAGTCAGTAT :::::::::::::::::::::::::::::::::	630 actccagaag1 ::::::::: actccaaaag1 660	640 CCAGTATGTGT.::::: CCAGTATGTGT. 670	650 FAGTTGTGTAT ::: FAG	660 GTTTTTTAA	670 CTTT
1309	680 730 740 I309 ACTATAAAGCCATGCAAAATGACAAATCTATATTACTTTCTCAAAAATGGACCCCAAAGAAACTTTGATT	690 Saaatgacaaa	700 AATCTATATT <i>I</i>	710 ACTTTCTCAAA	720 AATGGACCCCA	730 AAAGAAACTTT	740 GATT
CLAUD8							!
I309	750 760 770 780 790 800 810 I309 TACTGTTCTTAACTGCTTACAGGAACTGTGCATCAGCTATTTATGATTCTATAAGCTATT	760 SCCTAATCTTA	770 ATTACAGGAAC	780 STGTGCATCAO	790 SCTATTTATGA	800 ATTCTATAAGC	810 TATT
80114.T		 	 	! ! ! ! ! !	 	 	

Fig. 121

820 830 840 850 860 870 880 I309 TCAGCAGAATGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGT		900 910 920 930 940 950 ACTCTTTTTATCATTCAAAATGACATTGCTAAAGACTGCATTATTTTACTAC		970 980 990 1000 1010 1020 CGACATAGCATTATGATGAGTGTAACATTTATATCTCACATAGAGACATG		1040 1050 1060 1070 1080 1090 ATTTAAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTT		1100 1110 1120 1130 1140 1150 1160 I309 TCAGGGAAATCATGGATAGGGTTAGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGT	
830 840 PATTAAACCCAATGC		900 STCTTTTATCATTT		970 SACATAGCATTATGT		1040 TTTAAAATGAAATGC		1110 SATAGGGTTGAAGAA	
820 TCAGCAGAATGAGAT		890 I309 GGTTCAAGCATCTAC		960 I309 TGTAATTTCTCCACG		1030 CTTATATGGTTTTAT		1100 TCAGGGAAATCATGG	
1309	CLAUD8	1309	CLAUD8	1309	CLAUD8	1309	CLAUD8	1309	

Fig. 12C

1170 1180 1190 1200 1210 1220 1230 I309 CCTCCATTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTG	CLAUD8	1240 1250 1260 1270 1280 1290 1300 I309 ATATGCTGTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTT	CLAUD8	1310 1350 1370 1340 1350 1360 1370 I309 TTCTTGTGTATTAAATTTAAAAAGCAGATATTTTGTCAAGGGGGTTTGCATTCAAACTGCTT	CLAUD8	1309 TTCCAGGGCTATACTCCAGAAAAAAGATAAAAGTGTGTGATCTAAGAAAAAAGTGTTTTAGGAAAGTGGGAAAGTGAAAAAA	CLAUD8
0 AGGCTTTAATCAGC		0 AAATCCTAACTTCT		0 AAAGCAGATATTT		0 AAAGTGTGATCTAA	 - - - - - - -
1210 ATTGTAAAGGAA		1280 TTATCCTCTTC		1350 GTCAAGGGGCT		1420 GAAAAAGTGAT	
1220 AATTGAATGGC		1290 TCCCAGAGGCT	 	1360 TTGCATTCAAA		1430 GGTTTTAGGAA	
1230 TTTCTG		1300 TTTTTT		1370 CTGCTT		1440 AGTGAA	

Fig. 12F

1309	1450	1460	1470	1480	1490	1460 1470 1480 1490 1500 1510	1510
	AATATTTTTGTTT	TGTATTTGAAG	SAAGAATGATG	CATTTTGACA	AGAAATCATA	TTGTATTTGAAGAATGATGTTTTGACAAGAAATCATATATGTATG	TATAT
CLAUD8				} ! ! ! ! !			
1309	1520	1530	1540	1550	1560	1530 1540 1550 1560 1570 1580	1580
	TTTAATAAGTATT	GAGTACAGACT	TTGAGGTTTC	ATCAATATAA	ATAAAAGAGC	TGAGTACAGACTTTGAGTTTCATCAATATAAATAAAAAGAGCAGAAAAATATGTCTT	GTCTT
CLAUD8					 		-
1309	1590	1600	1610	1620	1630	1600 1610 1620 1630 1640 1650	1650
	I309 GGTTTTCATTTGCT1	ACCAAAAAAA	Saacaacaaa	AAAGTTGTCC	TTTGAGAACT	TACCAAAAAAACAACAAAAAAAAATTGTCCTTTGAGAACTTCACCTGCTCCTAT	CTAT
CLAUD8				 		 	-
1309	1660	1670	1680	1690	1700	1670 1680 1690 1700 1710 1720	1720
	GTGGGTACCTGAGTO	XAAAATTGTCAT	TTTTGTTCTG	TGAAAAATAA	ATTTCCTTCT	CAAAATTGTCATTTTTGTTGTGAAAAAAAATTTCCTTCTTGTACCATTTCTGT	CTGT
CLAUD8						 	
1309	1730	1740	1750	1760	1770	1760 1770 1780 1790	1790
	TTAGTTTTACTAAA	ATCTGTAAATACTGTATTT	STGTATTTTC	TGTTTATTCC	AAATTTGATG	TCTGTTTATTCCAAATTTGATGAAACTGACAATCCA	TCCA
CLAUD8							!

Fig. 12Q

1860	TTATATT
1850	SCTTTATACA1
1840	STTCTATTT
1830	TAAATGAATGT
1820	ICTGTCTAGCTT
1810	GTGTCGACGT
1800	ATTTGAAAGTTT
	309

CLAUD8 --

CLAUD8 ------

Fig. 12R

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COFFEE OF CHARLE

70 31 31 81 60	0	O.H.:HO	
VYDS :::: IYDS	140 PVSWV ::::: PVSWV 130	210 QRSFH :.:.: QKSYH 200	
10CK :-:: 10CK	.::: .v.r.i	HRTT :::: HRTT	
60 .::: .NIRI 50	130 'ITGL' :::. ITGM'	200 SVPSI :::: SIPSI	
MRH <i>P</i> .:.: .VRQ <i>P</i>	H · H H · H H · H	YRYS :::: YRYS	
WMNC:::	TAGI :::: TAGI	RSNS • • • • • • KSSS	
50 60 7C WEGLWMNCMRHANIRMQCKVYDSI ::::::::::::::::::::::::::::::::::::	120 RILL :::: HILL	190 CCTEI ::.:	
FENR	NVKSI .::. KVKAL	CCVE	
40 NIVVI :::: NIVVI 30	110 :TGDDE1 ::::: :TGDNE1	180 .GGALFG ::::: 'GGALFG	
TESP TENN	110 'RCTGD ::::: 'RCTGD	180 .IAGGA. :.::: .IVGGA.	
VSAE::::	::::	'ALVI :::: 'ALVI	
20 30 40 50 60 70 LVLGGVGMVGTVAVTIMPQWRVSAFIESNIVVFENRWEGLWMNCMRHANIRMQCKVYDSL ::::::::::::::::::::::::::::::::::::	90 100 110 120 140 LMCAASVLAFLAFMTAILGMKCTRCTGDDENVKSRILLTAGIIFFITGLVVLIPVSWV :::::::::::::::::::::::::::::::::::	160 170 180 200 200 210 VDVALKRELGEALYIGWTTALVLIAGGALFCCVFCCTERSNSYRYSVPSHRTTQRSFH :.:::::::::::::::::::::::::::::::::::	
VT IM : : : : VTVM	A FMT ::: A FMM	ALYI :::. ALYL	
0 GTVA :::: GTVA	O LAFL :: MSFL	0 ELGE ::::	
20 /GMVG ::::: /GMVG	90 AASVL :::::	160 ALKRE : ::: AQKRE 150	
71.GG7 ::: 71.GG7	SLMCZ SLMCZ	CVDVZ	SQYV
10 IAAL\ : :LE	80 JALSPDLQASRG ::::::::::::: JALSPDLQAARG	150 ANSIIRDFYNPL::.::	220 KRSPSIYSKS :.::::::
ALON	PDLÇ :::: PDLÇ	IRDE	SPSI
MATY 	80 90 100 110 120 130 140 LALSPDLQASRGLMCAASVLAFLAFMTAILGMKCTRCTGDDENVKSRILLTAGIIFFITGLVVLIPVSWV :::::::::::::::::::::::::::::::::::	ANSI ::.: ANAI	220 AEKRSPSIYSKSQYV . :.:::::::: TGKKSPSVYSRSQYV 210
10 20 30 40 50 60 70 CLAUD8 MATYALQMAALVLGGVGMVGTVAVTIMPQWRVSAFIESNIVVFENRWEGLWMNCMRHANIRMQCKVYDSL ::::::::::::::::::::::::::::::::::::	80 90 100 120 120 140 CLAUD8 LALSPDLQASRGLMCAASVLAFLAFMTAILGMKCTRCTGDDENVKSRILLTAGIIFFITGLVVLIPVSWV :::::::::::::::::::::::::::::::::::	150 CLAUD8 ANSIIRDFYNPL :::::::::: I309 ANAIIRDFYNSI 140	CLAUD8
CLA	CLA	CLA	CLA

Fig. 12

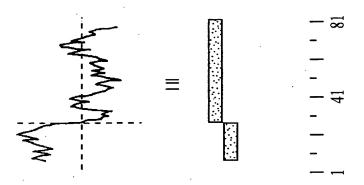
1309	LFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGL 40	
hCPE	MASMGLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGL 50	
mCPE	MASMGLQVLGISLAVLGWLGIILSCALPMWRVTAFIGSNIVTAQTSWEGL 50	
rRPV	.MSMSLEITGTSLAVLGWLCTIVCCALPMWRVSAFIGSSIITAQITWEGL 49	
1309	WMNCVRQANIRMQCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAIL	
NCPE MCPE	WANCVVQSTGQMQCKVYDSLLALPQDLQAARALVIISIIVAALGVLLSVV 100 WANCVVQSTGQMQCKMYDSMLALPQDLQAARALMVISIIVGALGMLLSVV 100	
rRPV.	. WMNCV. QSTGQMQCKMYDSLLALPQDLQAARALIVVSILLAAFGLLVALV 98	
I309	I309 GMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIPVSWVANAIIRDFYN 140	
hCPE	GGKCTNCLED.ESAKAKTMIVAGVVFLLAGLMVIVPVSWTAHNIIQDFYN 149	
MCPE	GGKCTNCMED.ETVKAKIMITAGAVFIVASMLIMVPVSWTAHNVIRDFYN 149	
rRPV	GAQCTNCVQD.ETAKAKITIVAGVLFLLAAVLTLVPVSWSANTIIRDFYN 147	
I309	SIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSYRYSIP 190	
hCPE	PLVASGOKREMGASLYVGWAASGLLLLGGGLLCC.NCPPRTDKPYSAKYS 198	
MCPE	PMVASGOKREMGASLYVGWAASGLLLLGGGLLCCSCPPRSNDKPYSAKYS 199	
rRPV	PLVPEAQKREMGTGLYVGWAAAALQLLGGALLCCSCPPREKYAPTKILYS 197	
I309	SHRTTQKSYHTGKKSPSVYSRSQYV 215	
hCPE	AARSAAASNYV209	
mCPE	AARSVPASNYV210	
rRPV	APRSTGPGTGTGTAYDRKTTSERPGARTPHHHHYQPSMYPTRPACSLASET 248	

Fig. 12T

CGAGCGGCCGCCCGGGCAGGTCAGACATGGGCCAAGGAGCCAGAGGCCGTCCGGGGGTCTGTGAGTTGAGGCCG 79

18	137	38	197	28	257	78	317
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Ν		ഗ	TCT	ഗ	ICC	¥	TAC
	GCA	ப	GAA	Σ	ATG	വ	೮೦೦
M		ტ	GGA	H	CTG	~	AGG
Н		ᇤ	TTT	Ω	GAC	>	GIC
됴		⊣	ACC	Ŀ	GAG	ഥ	GAA
ഗ	_	⊢	ACT	Ъ	သသ	Ы	CCT
ы		ഥ	GAG	Ω	GAC	Н	CTG
	AGC	⊡	GAG	ပ	TGT	>	GIC
	DDB 1	₽	ACA	ပ	TGC	X	\mathtt{TAT}
	ATA	д	CCC	æ	CGA	പ	CCT
	999	\triangleright	GIC	~	CGA	ഗ	ICC
	ATG		999	ပ	TGT	>	GTT
	ATC	Ĺτι	TTT	ტ	299	Д	CCT
	GIC	>	GTG	×	AAA	A	CCC
	; AGG	П	CTT	Ы	သသ	ø	CAG
Σ	ATG	വ	CCT	ᆸ	CIC	>	GIC
	CAGG	ᆸ	CTT	出	CAT	E⊣	ACG

Fig. 13A



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FIG. 13B

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[고	TTT	>	GTT	ഥ	TTT	Н	ATT	ပ	TGT	⊡	GAA
Н	ATC	Н	ATT	Н	ATT	ტ	GGA	X	AAA	Σ	ATG
Ц	CII	X	TAT	⊢	ACT	ы	CII	H	ACA	Ы	CTA
Н	ATT	X	TAT	ы	CIC	Н	CII	闰	GAA	ഥ	TIC
ഥ	TTC	ပ	TGT	വ	သသ	Ц	CII	A	GCA	×	TAT
ტ	GGA	ഗ	TCT	ပ	TGC	⊢	ACT	ഗ	AGT	~	AGA
>	GTT	Σ	ATG	>	GTT	ц	CIL	ĸ	AGA	Σ	ATG
Λ	GTT	а	CCA	M	$_{ m TGG}$	Λ	GTT	z	AAC	ĸ	AGA
Н	ATT	ပ	TGT	ഥ	TTC	Н	ATA	പ	CCA	ပ	TGT
ĸ	AGG	X	AAG	Λ	GTA	₽	ACT	Н	CAC	Ŀ	GAA
X	TAT	⊣	ACC	₽	ACT	н	ATA	ഥ	$_{ m TTT}$	ĸ	AGA
Н	TTA	Z	AAT	П	${ m TTG}$	ഗ	AGT	ഗ	AGT	н	CTA
洒	TTC	Ø	CAG	Н	ATA	н	ATC	ტ	999	Λ	GTT
闰	GAA	ტ	GGA	ტ	999	വ	CCI	×	TAT	വ	CCA
Σ	ATG	×	AAG	ы	TTG	н	ATA	X	TAT	ĸ	AAA
	4AGT	Н	ATT	⊢	ACT	ഥ	TTT	>	GTT	ტ	GGA
	TGTACTTGTATAAGT	Z	AAT	ტ	299	X	TAT	Н	ATT	Ω	GAT
	ACTT(Ĺτι	TTT	Ы	CTG	Ω	GAC	ы	CTT	Н	ATT
	TGT?	Ŀų	TTT	Λ	GTA	ы	CCA	ᅜᅫ	TTT	臼	GAA

Fig. 14A

AAAAAAAAAAAAAAAAAAAAA

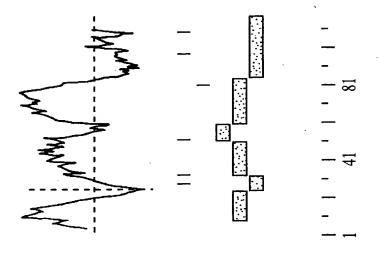


FIG. MB

				8/361			
8 8	28	48	68	88	108	128	148
	128	188	248	308	368	428	488
C.	E	N	A	T	K	D	K
	GAA	AAT	GCA	ACA	AAA	GAT	AAG
F	E		Q	K	R	V	T
; TTT	GAA		CAA	AAG	AGA	GTG	ACC
CIG	N	E	M	M	W	A	F
	AAT	GAA	ATG	ATG	TGG	GCT	TTC
L	E	I	E	I	ტ	A	K
	GAA	ATA	GAA	ATC	ტტ	GCT	AAA
L	T ACG	E	R CGG	E	P	R CGA	L
L	M ATG	L	I ATT	L	CIC	A GCA	P
R	R	S	K	T	T	M	TACT
GGC	CGG	TCT	AAA	ACC	ACC	ATG	
K	V	Y	D	N	Y	D	V
AAG	GTC	TAC	GAC	AAC		GAT	GTC
M ATG	L TTA	F	D GAT	S	3 3 3 3	P	K AAA
CGGACGCGGTGGCGCGCGCGCAGCTGAAGAAAGAGAGAGA	P CCC	Q CAG	I ATA	D	Y TAT	TACT	S AGC
AGAG	F TTT	N AAC	L	L CTG	Q CAG	Y TAT	W TGG
AGGAA	A GCA	L	S AGT	K AAA	G GGC	N AAC	V GTG
CTGA	S	Y	R	G	V	I	E
	TCT	TAT	AGG	GGA	GTG	ATA	GAA
GCAG	S	A	N	T	D	I	L
	TCT	GCA	AAT	ACT	GAT	ATA	TTA
GTGG	F	Q	K	V	P	R	G
	TTT	CAG	AAG	GTG	CCT	AGA	GGT
ACGC	T	A	S	T	V	m Y	E
	ACA	GCT	AGC	ACA	GTG	TAC	GAA
99295	I ATA	L CTG	Q CAA	Γ	ტ ტტტ	T ACC	O CAA
GTGG	F TTT	Q CAA	V GTT	G GGA	C TGT	CIC	I ATC
ອນອນ	F TTC	M ATG	L	F TTT	R AGG	N AAC	A GCT
CGGA	L TTG	N AAT	H CAT	F TTT	P	Y TAC	E GAG

Fig. 15A

				9/361			
168	188	208	228	248	268	288	308
548	608		728	788	848	908	968
$^{ m C}$	GGT	F	N AAT	L	A GCT	I ATC	Y TAT
R	P	G	S	P	P	A	Y
CGG		GGA	TCC	CCA	CCT	GCT	TAT
GG.T	G	A	H	Y.	V	D	I
	GGT	GCA	CAC	TAC	GTA	GAC	ATC
H	P	G	S	K	K	F	R
CAT	CCT	GGA	TCT	AAA	AAG	TTT	AGG
V GTC	P CCT	D GAT	L	R AGA	P	T ACT	W TGG
R CGA	F TTT	K AAG	ტ ტტტ	P	Γ	Γ	L CTA
T	A	T	L	D	G	D	H
ACT	GCC	ACC		GAT	GGT	GAC	CAC
R AGG	H CAT	W TGG	A GCA	L	G GGA	P	R AGG
F	G	N	H	S	Y	D	ტ
TTT	GGC	AAC	CAT	TCC	TAT	GAC	ტტე
A	L	E	G	V	I	C	K
GCC		GAA	GGT	GTC	ATC	TGT	AAA
I	V	D	F	Y	S	A	F
ATT	GTG	GAT	TTT	TAT	TCC	GCC	TTT
M	G	E	E	N	Q	H	F
ATG	GGA	GAG	GAA	AAT	CAG	CAT	TTC
I	L	D	H	P	I	P	M
ATC	TTG	GAT	CAT	CCA	ATC		ATG
D	P	F	A	F	G	I	V
GAC	CCC	TTT	GCT	TTC	GGA	ATA	GTA
A	G	H	A	M	N	T	E
GCA		CAT	GCT	ATG	AAT	ACT	GAA
I	D	T	V	L	I	P	R
ATT	GAT	ACT	GTG	TTG	ATC		AGA
ტ	F	D	L	A	D	E	R
ტტტ	TTT	GAC		GCC	GAT	GAA	CGC
K	Y	G	F	T	D	K	${ m F}$
AAG	TAT	GGT	TTT	ACA	GAT	AAG	
S	R	G	$_{ m L}$	Q	Q	P	T
TCA	CGC	GGT		CAA	CAG	CCA	ACT
I ATT	P	L	N AAC	D GAT	S TCT	K AAG	T ACA

Fig. 15B

CGFEGICA CARPA

130/361 368 1148 1268 348 1088 408 388 1208 1328 1388 468 1448 D GAT F ITC GGT TACC K AAA PCCA A GCT I ATT A GCT N AAC L TTA AAA GAC N AAC E GAA A GCT \bowtie Д E GAA T ACA AGA P CCA M ATG Y TAC K AAA D GAT 召 L D GAT H CAT T ACA TACC C TGC V GTT E GAA I ATC T ACC K AAA Q CAA S TCT R CGT FTTT CAA PCCA F TTT S TCC K AAG TACC I ATC FTTT O CAA W V GTT K AAA D GAT M ATG S AGT K AAG W TGG TACT F L CTG PCCC $_{\rm TGT}^{\rm C}$ E GAA IATC S TCA V GTC S TCA I ATT Y TAT D GAT GGA G GGA N AAT K AAG D GAT A GCC TACT A GCT F TTT PCCT R CGT R AGA I ATT D GAT P CCA A GCA R AGG F TTT S AGC L TTA R AGA L TTG D GAT $\overline{\mathbf{W}}$ H M ATG FTTC I ATC I ATA E GAA P V GTC C TGC K AAA F TTT N AAC K AAA \overline{W} V GTA R CGA F TTT A GCT F K AAG E E GAG Y TAT TACC I ATT V GTG FTTC Y TAC GGA V GTG G GGC R AGA I ATT V GTT GGA D GAT A GCA R AGA R CGT GTG Q CAG K AAA N AAT \triangleright TACG I ATC GGA Y TAC K AAG FTTT P A GCT TACA I ATC ATG CCA TIC F TTC Q CAA Q CAG Σ Д ഥ LCTG W TGG TTTY TAC GGA FITC K AAG ſτι

Fig. 15C

488 508 1568 K AAG N AAC I ATA K AAA g ggC L G GGA L TTG S TCA H CAT H CAT V GTT A GCA I ATT K AAA GGT GAA FTT K AAG I ATT N AAC FTTT I ATC L TTG D GAT S AGC FTT L TTA G GGT S AGT K AAG F TTT H CAT S TCA s TCC Y TAT N AAC $\frac{1}{1}$ K AAG I ATA

* TAA CAA Y TAT I ATT S TCT TACT

1665 **ATTCATAGACCTAAAATAAACCTCAACAGGTCTTTTAATATATAATTCTGCTTCAAAATAGAATAAAACCATTCTTTAAC** 131/361

514 1586

AACAAAAAAAAAAAAA

Fig. 151

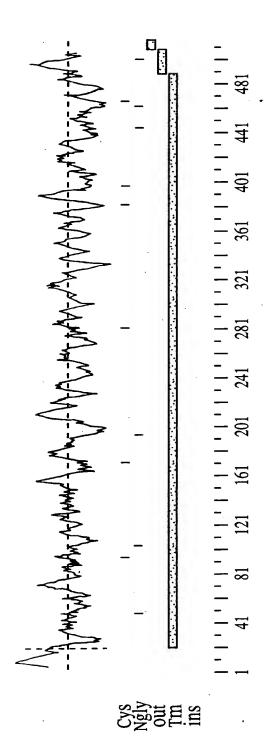


FIG. 15E

								133/3	61						
13	09		120	53		73	240	93	0	113	9	3	420	153	∞
E	ACA	Ø	225	w	AGC	E	ACA	>	GTA	X	TAC	X	AAA	\triangleright	GTT
нΪ	ATA	Ц	CIG	Ø	CAA	ı	TTG	ტ	999	₽	ACA	Ø	CAG	ტ	999
[편 [LLI	Ø	CAA	>	GIC	ტ	GGA	Ŋ	TGT	П	CII	н	ATT	×	AAG
z	AAT	z	AAC	[五	TTT	ĮΤΙ	TIC	М	AGG	ഗ	AGC	Ø	GCT	ഗ	ICC
	GI'I'	Z	AAC	H	CAT	ഥ	$_{ m LLL}$	Д	သသ	∺	TAC	ഥ	GAG	н	ATA
Z E	A'I'G	ы	GAG	ഗ	AGT	А	GCA	>	GTG	X	AAA	Ω	GAT	ĸ	AGG
L E	CIG	臼	GAG	ტ	GGG	Ø	CAG	凶	AAA	ሺ	AGA	>	GTG	₽	ACC
လ မို	ICI	Z	AAT	ഥ	GAA	Σ	ATG	Σ	ATG	M	$^{ m IGG}$	Ω	GAT	Ĺτι	$_{ m TTT}$
LI E	CIG	X	AAA	Н	ATA	ഥ	GAA	Н	ATC	ტ	999	Ø	GCT	⊢	ACG
LJ (CIL	Ω	GAC	ഥ	GAA	以	CGG	Ø	929	വ	CCI	Д	CCA	ы	CIG
ပ ပ (J.5.T.	X	AAG	ᄓ	CII	ᆸ	CTT	Н	CTT	니	CIC	H	ACA	Д	CCA
₩ F	AAG	凶	AGG	ഗ	TCI	又	AAA	H	ACA	₽	ACA	Σ	ATG	₽	ACT
∑ E	A.I.G	Ω	GAC	×	TAC	ტ	GGA	Д	GAC	×	TAC	Q	GAT	>	GIC
f (4GGA	Д	CCA	Ĺτι	TTC	Ω	GAT	Ø	TCA	ტ	299	Д	CCI	X	AAG
r F	4GAC4	വ	CCT	Ø	CAG	Ĺτι	TTT	Д	GAT	×	TAT	₽	ACT	ഗ	AGC
, , ,	GCTTTTAACTGAAGAGACAGGA	Ŀч	TTT	Z	AAC	Ы	CIC	Н	CIG	Ø	CAA	X	TAT	M	TGG
Ì	AAC'I'(Ø	GCA	П	CIC	Ω	AGT	X	AAA	ტ	999	Z	AAC	\triangleright	GTT
: : :	7.I.I.	Ø	GCT	¥	TAT	24	AGG	ტ	GGA	>	GTG	Σ	ATG	ø	CAA
(<u>.</u>	ഗ	ICC	A	GCA	Z	AAC	H	ACT	Ω	GAT	Н	ATA	ы	CTA
		П	CTT	Ø	CAG	×	AAG	Λ	GTG	ሲ	CCA	Ж	AGA	Ø	GCT

Fig. 15F

173 540	193	213	233 720	134/361 & 0 & & C C	273	293	302 927
D GAT	TACT	L	A GCC	D GAT	G GGA	R CGC	
F TTT	D GAC	F TTT	T ACA	D GAT	S AGT	F	
H CAC	G GGT	$_{ m L}$	Q CAA	Q CAG	P CCA	TACT	
R	G	N	D	S	K	T	
CGT	GGT	AAC	GAT	TCT	AAG	ACT	
PCCT	L	F	N AAT	L	T ACC	I ATC	
C	G	G	S	P	T	A	
TGT	GGT	GGG	TCC	CCA	ACC	GCT	
T	L	E	H	Y	V	D	
G	CTG	GAA	CAC	TAC	GTA	GAT	
9 66C	G GGT	GGG	S TCC	K AAA	K AAG	FTT	
H	P	D	L	S	P	T	
CAT	CCT	GAT	CIG	AGC	CCT	ACT	
V GTC	P CCT	K AAG	GGG	P CCT	P CCA	Γ	
G	F	A	L	D	S	T	
GGA	TTT	GCC	CTG	GAT	AGT	ACC	
T	A	I	S	L	G	CCC	R
ACA	GCC	ATA	TCT	CTG	GGA		AGG
R	H	W	H	S	$_{ m Y}$	D	
AGG	CAT	TGG	CAC	TCC		GAC	9
F	9	T	G	I	I	C	K
TTC	9	ACA	GGT	ATC	ATC	TGT	AAA
A	L	E	F	Y	S	A	F
GCA		GAA	TTT	TAC	HCC	GCC	TTT
I	V	D	E	N	Q	H	F
ATA	GTC	GAT	GAA	AAT	CAG	CAC	
M ATG	G GGA	E GAA	H CAT	CCC	I ATC	P	M ATG
I ATA	Γ	D GAC	A GCT	F	G GGG	E GAA	V GTT
D	P	F	A	M	D	S	E
GAT	CCT	TTT	GCT	ATG	GAT	TCT	GAA
A GCA	GGT	H CAC	V GTG	$_{ m L}$	I ATT	N AAT	R AGG

Fig. 15G

1279 1087 1167 1247 | CAAAGAAAACACCCCAAGGGCAACCTGCAGCCTCCACACATAAGCACATGCATTCACATGTATGCCACATATGTGA ACATGTAGGCACACATGCATGCATACCACAAACCACAAACTTAAGACTGAAACATGCTGATGGACACAGGTACCAGGACA **PCATTGATGAAATATTTTTGTGTTTAATGCAGG**

342 1399 1459 362 382 322 1339 402 579 F TTC E GAG L CTT PCCC $^{\rm C}$ V GTC S TCC CIC $^{
m Y}$ D GAT GAT G GGT A GCC TAT E GAG ≻ Ω I ATT D GAT PCCC GCA R AGG Ø ${
m F}$ L TTG D GAT R AGA W TGG E GAG င Tgc PCCC V GTC I ATT S TCT K AAA W TGG F TTT S AGC K AAG I ATC E GAG E GAA Y TAT A GCT Y TAT V GTG 999 GGA A GCC GGT R AGG R CGT V GTT A GCT I ATC A GCT F TTT R AGA V GTC I ATT Q CAA P CCA F TTT D GAT W TGG L CTT F TTT F S TCT D GAT TACC F TTC GGA Y TAC L CIC A GCT AAT K AAA Z V GTC E GAG T ACA R AGA P CCA R AGG Γ H CAC T ACA D GAT I ATC D GAT W TGG K AAA S TCT $_{
m L}$ s TCC CAT P CCA F TTT 田 H CAC GTT K AAA GAT W TGG > Ω

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Fig. 15H

422

I ATT

ഗ

Д

F TTC

C TGC

X

Н

24

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G

Ω

M ATG

Ø

Ø

Σ

 $^{
m F}$

AAG

ATA

I ATA

AGG

CAG

CCA

GGA

R AGA

GAC

GCA

GCA

ATG

Q CAA

GGA

CCA

-4 -4 1=0

462	482	502	5111
1759	1819	1879	1949
S	A	I	CAATAAATTCCACAAATAAACCAAAACAAATCTTTAACC
TCT	GCA	ATT	
N	K	S	TTTT
AAT	AAA	AGT	
T ACC	G GGA	F	AATC
K	K	T	AAACP
AAA	AAA	ACT	
I ATC	V GTC	L	CCAP
V	S	L	TAAP
GTG	AGT	TTG	
Q	V	S	CAAA
CAA	GTC	AGC	
T ACC	N AAT	$_{ m L}$	TCC
I ATC	F	R AGG	TAAAT
N	S	K	CAAI
AAT	TCA	AAA	
K	A	H	*
AAA	GCA	CAT	TAA
A	N	H	N
GCG	AAC	CAT	AAT
K AAG	$_{ m L}$	$_{ m L}$	YTAC
M	P	I	T
ATG	CCA	ATA	ACA
D	E	V	K
GAC	GAA	GTG	AAA
Y	N	T	T
TAT	AAC	ACA	ACA
E	C		L
GAA	TGT	GGC	CTG
F	$_{ m CTG}$	I	V
TTT		ATT	GTG
Q	F	S	H
CAA	TTC	TCA	CAT
R	\overline{W}	N	V
AGG		AAT	GTT
	Q F E Y D M K A K N I T Q V I K T N S 46 CAA TTT GAA TAT GAC ATG AAG GCG AAA AAT ATC ACC CAA GTG ATC AAA AAT 175	Q F E Y D M K A K N I T Q V I K T N S 46 CAA TTT GAA TAT GAC ATG AAG GCG AAA AAT ATC ACC CAA GTG ATC AAA ACC AAT TCT 175 F L C N E P L N A S F N V S V K G K A 48 TTC CTG TGT AAC GAA CCA TTA AAC GCA TCA TTC AAT GTC AGT GTC AAA GGA AAA GCA 181	Q F Y D M K A K N I T Q V I K T N A K A K N I K T N Y I K T N A X X Y X Y X

2269 2109 2189 2349 2429 2467 AGGTTTGATTCTCAGTACCCACATGGCAGTCCACAGCTCTCTGTAACTCCAGACCCAGGGAAATCTGATGCCCTCTCTGG TGAACTCTGCCTCAGGAAGACTCAAGAGTGGGAGAGAGATGACCCAGTGGTTAAGTGCACTGGCTGCTCTTTCAAAGGACCC AGTAAAATAATTGAGCCCAATTCTTTAGCATCAAGTTCTTACTCCTACTATATATCAGCTGGGTAACCAATAACCAGTTA a*aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa*a

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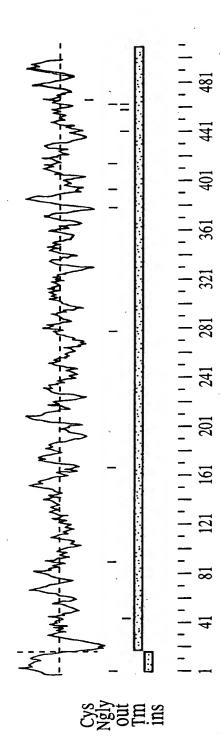


FIG. 151

COVECATO CTAPOL

O AIQE ::: AIQK O	0 NW-T .: . TWIA 0	270 AKPKE .:: TKPSG 70
13 AAVDE. .::: DVDE.	20 'DEDEI :::: 'DEDE'	27)KVPAK :: .:)KVTTK 270
DMARA::::::	GDTHF	O YGGLF YGSPF
120 INYTE .:::: MNYTE	190 GPGLG:::::	210 220 240 250 270 270 KDGAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYVSLDPRKYPLSQDDINGIQSIYGGLPKVPAKPKE :::::::::::::::::::::::::::::::::::
LTYRI ::::: LTYRI	HAFPF ::::: HAFPF	0 QDDIN ::::. QDDID
110 WRKYN ::::: WRKYS	180 LGVLG ::::: LGVLG	250 KYPLSQI :::::: KYPLSQI 250
YTLPG ::::: YTLPG	YFDGP :::: HFDGP	O SLDPR :::: SLDPS
100 VGQYG VGQYG 100	170 GRCPR: :.::: SWCPR: 170	240 FPNYVS: :::::: FPNYIS: 240
CGVPD	RTRVH :::::	0 2TALM ::::: 2TALM
90 MKTPR: : : : : MKVPR	160 IMIAF) ::::: IMIAF) 160	230 SHSNDQ :::::: SHSNDQ 230
TLEII .:.:)TLAII	GGIAD)	ALGL:
80 3KLDSN ::::: 3KLDSI 80	150 TKISF:::::	220 NHEFGH :::::: NHEFGH 220
LTVTC :::::	TPLKE: ::::::TPLTE	FLVA?
70 QAFFG : : : : : QAFFG 70	140 VWSKV :::::	210 KDGAGFNLFLVAAH ::::::::::: KDGEGFNLFLVAAH 210
REM : :: REM	GLE · : ·	KDG ::: KDG
human murine	human murine	210 220 240 250 270 270 human KDGAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYVSLDPRKYPLSQDDINGIQSIYGGLPKVPAKPKE :::::::::::::::::::::::::::::::::::
	80 GLTVTGKLDSNTLEIMKT ::::::::::::: GLTVTGKLDSDTLAIMKV 80	human REMQAFFGLTVTGKLDSNTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTYRIINYTPDMARAAVDEAIQE :::::::::::::::::::::::::::::::::::

Fig. 15K

DOFEDIBO CTTES

340 ENPRDKILV : :: :: :: ESPRDELLV 340	410	480 SFDINKEKA . : : : NVSV-KGKA 480	
320 IASFWPSLPADLQAAYE : :::::::::::::::::::::::::::::::::::	400 WCWRFDEMT(::::::: WCWRYDEMA(400	470 CKEPKNSSFC :.:::::: CNEPLNASFN	
320 FELIASFWPS::::::: FEFIDSFWPS:320	0 370 380 390 400 410 YPKSIHTLGFPGRVKKIDAAVCDKTTRKTYFFVGIWCWRFDEMTQTMDKGFPQ ::::::::::::::::::::::::::::::::::::	460 RIMRTNTWFQ ::: QVIKTNSWFL	
90 310 TTFRREVMFFKGRHLWRIYYDITDVEFE :::::::::::::::::::::::::::::::::::	380 KIDAAVCDKT ::::::: KIDAAVCDHD 380	450 EYNIKTKNIT :: .:.::: EYDMKAKNIT 450	
300 .VMFFKGRHLW ::::::::::	370 HTLGFPGRVK :::::::::: HTLGFPRRVK 370	440 FFFSRGSKQF .: : : : : LYFFHGSRQF 440	510 ILLKNTSIYQ .: .:. [VLTKTYN 510
290 LTFDAITTFRRE ::::::::::: LTFDAITTFRRE 290	360 AVLPDYPKSI .::::::: SVLPGYPKSI 360	430 VDAAFQYKGF :::.:::: VDAVFQHNGF 430	500 LSLFIFGIVHLLF:::::::::::::::::::::::::::::::::::
280 300 310 320 340 340 340 320 330 340 human PTIPHACDPDLTFDAITTFRREVMFFKGRHLWRIYYDITDVEFELIASFWPSLPADLQAAYENPRDKILV ::::::::::::::::::::::::::::::::::::	350 360 410 FKDENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDAAVCDKTTRKTYFFVGIWCWRFDEMTQTMDKGFPQ ::::::::::::::::::::::::::::::::::::	420 430 440 450 460 470 480 RVVKHFPGISIRVDAAFQYKGFFFFSRGSKQFEYNIKTKNITRIMRTNTWFQCKEPKNSSFGFDINKEKA :::::::::::::::::::::::::::::::::::	490 500 510 HSGGIKILYHKSLSLFIFGIVHLLKNTSIYQ :.:. ::::::::::::: NSIGTVILHHKRLSLLTFSIVHVLTKTYN 490 500 510
human E murine N	human F : murine F	human F : murine F	human F murine N

Fig. 15L

rozen oznaka

70 STTTTT :.: :	140 CAACTG ::::::	210 4GAATA :::::	280 ACTGGA :::::
60 TCTGCTTCT :::::::::	130 GAAAATATG(::.:: :. GAGAACAAC(200 TTCAAAGCAA : :::::: TCCAAAGCAA	270 GACTGGAAA! ::::::::: :GACTGGAAA!
40 GAGAGGAATGAAGCGCCTTCTGCTTCTGTT::::::::::	120 GGAAAATGAZ .:::::: .CAAAAATGAG	190 AATCATCTTG : . : : : : : : : : AGTCATTTTT	260 GATTGACAG1 ::::::::: GATTGACAG1
40 AAGAGAGGAA ::::::: GACAGGAA	110 TCCGGATGAC .: ::.:. ACAGGAAGGA	180 AATAGAAGGG :::::::::	250 3CATTTTTG :::::::: 3CATTTTTCG 230
30 40 50 70 CAGCTGAAGAAGGAATGAAGCGCCTTCTGCTTTTT :::::::::::::::::::::::	0 100 110 120 130 140 TCTGCATTTCCCTTAGTCCGGATGACGAAAATGAAGAAATATGCAACTG ::::::::::::::::::::::::::::::::::::	170 ACTCTCTTGA: ::::::::	240 3GAAATGCAA(:::::::::
20 ACGCGTGGG	90 TTCTTCTGCA: ::: :::: TTCCGCTGCA: 70	160 ACCAGTTCTZ :::::::: ACCAGTTCTZ	230 CAAAATTCGC ::: ::: AAAACTTCGC
10	80 CTTTATAACATT :::::::::: ITTTATAACACT 60	150 160 170 180 190 200 210 GCTCAGGCATATCTCAACCAGTTCTTCTTCTTCTTCTTCTTCTTCAAGCAATAA :::::::::::::::::::::::::::::::::	220 230 240 250 260 270 280 280 6GAGTCTCATAGATGCGAAAATGCAAGCATTTTTTTGGATTGACAGTGACTGGAAAACTGGA
human CGC murine	human GTT murine TAA	human GCT :: murine GCC	human GGA ::: murine GGA

Fig. 15M

350 ACC	:: 'ACA	360 370 380 400 400 420 CTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAAACTATACTCCGGATATGGCACGAGCTG :::::::::::::::::::::::::::::::::::	430 440 450 460 470 480 490 CTGTGGATGAGGTTTAGAAGTGTGGAGCAAAGTCACTCAC	::: GAT	500 520 530 540 550 560 TTCAAAGGGGATTGCATGATTGCTTTTAGGACTCGAGTCCATGGTCCTCGCTCTTTTTTT .::::::::::::::::::::::::::::::::::::
290 340 310 320 330 340 350 CTCAAACACCCTTGAGATCATGAGACACCCCAGTGTGGGGTGCCTGATGTGGGCCAGTATGGCTACACC	::::::::::::::::::::::::::::::::::::::	360 370 380 390 400 410 420 CTCCCTGGGTGGAGAAATACAACCTCACCTACAGAATAAACTATACTCCGGATATGGCACGAGCTG :::::::::::::::::::::::::::::::::::	CAA	::::: ::::::::::::::::::::::::::::::	500 520 530 540 550 560 TTCAAAGGGATTGCAGTCATGATTGCCTTTAGGACTCGAGTCCATGGTCGTGTCCTCGCTATTTT ::::::::::::::::::::::::::::::::::::
255	:::: TGGC 320	GCAC .::: ACAC	CAC	: :: TTAC 460	TCGC ::: TCGT 530
340 GTAT	::: TAT 3	410 ATGG ::::	7 480 AATT	.:. GTT 4	550 TCCT :::: TCCT
3 CAG	::.	4 !ATA! :::	4 688	·: GAC	550 GGTGTCCTCG ::::::::: GGTGTCCTCG 530
3660	:::: TGGGC 310	TCCGG::::::::::::::::::::::::::::::::::	ZACT	::::: CCACT 450	GTCGG : :: GCTGG 520
330 ATGTC	:::: IGTC 31	400 TACTC :::::	470 ACTCC	::::: CTCC 45	540 ATGG1 :::: ATGGC
33 IGA	.::	4 (IATZ ::::	4 CICA	::: ICA(54 CCA: :::
GGG	.:: ACC; 0	AAC: BAAC:	AAG	::::::::::::::::::::::::::::::::::::	510 520 530 540 GACATCATGATTGCCTTTAGGACTCGAGTCCATGG ::::::::::::::::::::::::::::::::::
0 GGT	:::. GGTA(300	0 ATAA :::: ATGA), GCA	:::: GCAA(440	0 TCGA(. :: AGGA(510
320 TGGG	::: Idd	390 ATAA: :::: ATAA	460 GGAG	: : : GGA	530 GACT :::. GACA
GTG	::: 1GTG	: : : : : : : : : : : : : : : : : : :	TGT	: : ;	TAG :: :CAG
CAG	::: CAG) TTAC ::: \TTAC	30C	::: AAG' 430) CCTT' :: CATT' 500
310 2ACC	.:. 1900	380 2ACC' :: FACA'	450 LTAG	:: CTAC	520 FTGC : . : : FAGC
AGA(::::::: ATCATGAAAG: 280	CCT(GGT	: : 3CT(IGA: ::: IGA:
TGA	::: TGA 280	.: .: .:	GAA	.:: AAA(420	TCA: : : TAA: 490
300 TCA	TCA	370 ATA(:::	440 CAA	::. CAG	510 ACA:::
AGA	:: ICGA	:::	ATC	:: 'ATT	CAG :::
TTG	::::::::::::::::::::::::::::::::::::::	360 CTCCCTGGGTGGAGAA ::::::::::::::: CTCCCTGGGTGGAGAA	GCT	::::::::::::::::::::::::::::::::::::::	500 FTCAAAGGGGATTGCA ::::::::::::: ATCCAAGGGGGTTGCA
290 ACCC	1 : : : 4 CAC	360 GGTG :::: GGTG	430 TGAG	: : : : IGAG	500 6669 1 : : : .
AAC7	.:::	7. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	4 3GAT	::::: 3GAJ	24AGG
rca.	::: TTCAC 260	CTCC	JG IGT(::: ATGTC 400	TTCA2 .:: ATCC2 470
ຽ			ក់ ប៊	e A. 4(
human	murine	human murine	human	::::::::::::::::::::::::::::::::::::::	human murine
hu	ш	hu mu	hu	пш	hu mu

Fig. 15N

human	570 GATGGTCCCT	0 TTGGGAGTGC	580 GCTTGGCCA	590 TGCCTTTCC	600 rccreercc	610 3GGTCTGGGT	570 580 590 600 610 620 630 6ATGGTCCTCCTGGTCCGGGTCTGGGTGACACTCATTTTG	630 TTG
murine	:::::: GATGGTCCT	:::::::	::::::::::::::::::::::::::::::::::::::	TGCCTTTCC	::::::: CTCCTGGTCT	::::::::::::::::::::::::::::::::::::::	murine GATGGTCCTCTGGGAGTCCTTGGCCATGCCTTTCCTCCTGGTCTGGGTCTAGGTGGTGACACTCACT	j
	540	550	260	570	580	590	009	
	640	0	650	099	670	680	069	
human	ATGAGGATGAAAACTG	AAAACTGGA-	CCAAG	GATGGAGCA	GATTCAAC	FTGTTTCTTG	CCAAGGATGGAGCAGGATTCAACTTGTTCTTGTGGCTGCTCATGAATT	TT
mוריות		::::::::::::::::::::::::::::::::::::::	::::: ::::				######################################	: E
) 	610	620	630	640	650	099	670	1
	700	710	720	730	740	750	160	
human	TGGTCATGC	ACTGGGGCT(CTCTCACT	CCAATGATC	AAACAGCCT	IGATGTTCCC	TGGTCATGCACTGGGGCTCTCTCACTCCAATGATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTG	ĐI:
mirine	::::::::::::::::::::::::::::::::::::::					::::::::::::::::::::::::::::::::::::::	STOCOLOUR STATEMENT OF THE ST	[-]
	089	069	700	710	720	730	740)
	770	780	790	800	810	820	830	
human	GATCCCAGA	AAATACCCA(CTTTCTCA	GGATGATAT	CAATGGAAT	CCAGICCAIC	GATCCCAGAAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTA	TA
-				••				••
murine	GATCCTAGC 750	AAATACCCA(760	CTTTCTCA 770	GGATGATAT. 780	rgatrgggat 790	CCAGTCCATC 800	murine GATCCTAGCAAATACCCACTTTCTCAGGATGATATTGATGGGATCCAGTCCATCTATGGAAGTCCACCTA 750 760 770 780 790 800 810	TA

Fig. 150

human murine	840 AGGTACCTGCTAAGC :::::::::::: AGGTAACCACCAAGC 820 830	850 3CTAAGCCAAA .: ::::::	860 CAAAGGAACCCACT ::: :: :: CAAGTGGAAATTCT 840	870 ACTATACCCCATG .::::::: TCTGAACCCCACG 850	880 GCTGTGACCC1 ::::::::: GCCTGTGACCCC 860	840 860 870 890 900 human AGGTACCTGCTAAGGAACCCACTATACCCCCATGCCTGTGACTTTGACTTTTGACGCTAT ::::::::::::::::::::::::::::::::::::	900 TTGACGCTAT :::::::: TTGATGCTAT 880
human	910 CACAACTTI	920 rccgcagaga	930 AGTAATGTTCI	910 920 930 940 CACAACTTTCCGCAGAGAAGTAATGTTCTTTAAAGGCAGG-		 	
murine	::::::::::::::::::::::::::::::::::::::	:::::::: 	::.::::: \GTTATGTTCT 910	::::::::::::::::::::::::::::::::::::::	: GTAAACCTAT7 930	:::.::::::::::::::::::::::::::::::::::	TCCAGCTTCT 950
human	 		 		; ; ; ; ; ;	 	
murine	TATAAAGATGTTTTT 960 970	rGTTTTTTT 970	TTCAAAGGAT 980	CTCCGGATAA 990	ACAGTCTTCT? 1000	TTTTTTCAAAGGATCTCCGGATAAACAGTCTTCTACTCAGCTAGAAAGCCAGTTG 980 990 1000 1010 1020	AAAGCCAGTTG 1020
human							
murine	CTGAGCATC	STACCAGTACA 1040	TCAGCAAGAC 1050	ATTCTTCCTC 1060	AAGAAACAATC	murine CTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCCTCAAGAAACAATGTAGAAAACAATCAAAGAAAA 1030 1040 1050 1060 1060 1070 1080 1090	ATCAAAGAAAA 1090

Fig. 15F

1110 GCTGTCTTG :::::: TCTGTCTTG 40	1180 CAGCCGTCT ::::::::: CAGCCGTCT	1250 AATGACCCA .:::::: .GATGGCACA	1320 GTTGATGCT :::::: GTGGATGCT 50
11 3ATATGC :::::: 3ATATTC 1440	11 AGATGCA .::::: IGATGCA 1510	12 3ATGAAA! ::::::: 3ATGAGA! 1580	13 rccgrgr ::::::: rccgrgr 1650
1100 TGATCAGAGC : :::::: TCATCAGGGC	1170 GAAGAAAAT? :::::::: GAAGAAAATT	1240 TGGAGGTTTC ::::::: TGGAGGTATC 1570	1310 GAATCAGTAT :::: : : GAATTCGCCT
1090 AACTTCTGGA ::::::::	1160 CAGGACGTGT ::::::::	1230 CATTTGGTGC ::::::::	1300 CACTTTCCTG .::: :::: FGCTTCCCAG
1080 'AAAGATGAA <i>Z</i> :::::::::: 'AAAGATGAG <i>Z</i>	1150 TAGGTTTTCC : ::::::	1220 CTTTGTGGGC ::::::::::::::::::::::::::::	1290 GTGGTAAAAC .::::. ATAATAAAG1
1070 1080 1090 1100 1110 TTCTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGTCTTG : ::::::::::::::::::::::::::::::::::	1140 1150 1160 1170 1180 ICCATCCATACATTAGGTTTTCCAGGACGTGTGAAAAAAAA	1210 1250 1230 1240 1250 SAAAAACCTACTTTGTGGCCATTTGGTGCTGGAGGTTTGATGAAATGACC :::::::::::::::::::::::::::::::::::	1280 1300 1310 1320 ATTCCGCAGAGAGGTAAAACACTTTCCTGGAATCAGTATCCGTGTTGATGC ::::::::::::::::::::::::::::::::::::
GA GC	L: L:	1200 ACAA(:::: ACAA(30	
1050 1060 GAACCCCAGAGATAA .:.::::::::::::::::::::::::::::::::	1120 1130 CCAGATTATCCCAAA ::::::::::::::::::::::::::::	1190 GTGATAAGACC ::::: : . : GTGATCATGAT	1260 1270 AACCATGGACAAAGG :.::::::::::::::::::::::::::::::::
human murine	human murine	human murine	human murine

Fig. 15R

	GCAGCCTCCACATAAGCACACATGCATTCACATGTATGCCCCACATATGTGA 1120 1130 1140 1150		GCATGCATACCACAAACTTAAGACTGAAACATGCTGATGGACACAGG 1190 1200 1210 1220 1230	960 970 CACCTATGGAGGATCTATTATGATATCA	ATGAAATATTTTGTGTTTAATGCAGGCACTTATGGAGGGTCTACTCTGATATTG 1260 1270 1280 1290 1300	1000 1010 1020 1030 1040 ATTAATTGCTTCTGGCCATCTCTGCCAGCTGCAGCTGCATACGA .::.:::::::::::::::::::::::::::::::::
1			ACTGAAACA1 1220	960 CTATGGAGGA':	TTATGGAGGG	1010 1020 1030 TTCTGGCCATCTCTGCCAGCTGATCTG ::::::::::::::::::::::::::::::::::::
	 ACACATGCAT 1140		CAAACTTAAG 1210	CAC	ATGCAGGCAC 1280	1020 CCATCTCTGC :::::::::
	ACACATAAGC	 	CACAAACCA(1200		TTGTGTTTA 1270	1010 TTCATTCTGG(:::::::: TTCCTTCTGG(
	GCAGCCTCCA		GCATGCATAC 1190		ATGAAATATI 1260	1000 ATTAATTGCT .::::::::
	murine CACCCAAGGCAACCT		murine ACATGTAGGCACACAT 1170 1180		murine TACCAGGACATCATTG 1240 1250	990 FTGAGTTTGA :::::::::
950	1		ne ACATGTA 1170		ne TACCAGO 1240	980 n CGGATG: : :.:: ne CTGGTGC
ל הפשניל	murin	human	murir	human	murir	human murin

Fig. 15Q

1350 1360 1370 1380 1390 GGATTCTTCTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAA ::::::::::::::::::::::::::::::::	1420 1430 1440 1450 1460 CATGAGAACTAATACTTGGTTTCAATGCAAAGAACCCAAAGAACTCCTCATTTGG :::::::::::::::::::::::::::::::::	1490 1500 1510 1520 1530 GGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCTTG .:.::::::::::::::::::::::::::::::::	1580 1590 1600 ACTICTATITATCAATAAATTCATAGACCTAA :::::::::::::::::::::::::::::::::
1330 1340 1350 1360 1370 1380 1390 human GCTTTCCAGTACAAGGATTCTTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAA : :::::::::::::::::::::::::::::::::	1400 1410 1420 1430 1440 1450 1460 human AGAATATTACCCGAATCATGAGAACTTAATACTTGGTTTCAATGCAAAGAACCAAAGAACTCTCATTTGG :::::::::::::::::::::::::::::::::	1470 1480 1500 1520 1530 TTTTGATATCAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAGAGTTTTAAGCTTG : : : : : : : : : : : : : : : : : : :	1540 1550 1560 1570 1580 1590 1600 TTTATTTTTGGTATTGGTGAAAACACTTCTATTTTATCAATAAATTCATAGACCTAA : ::::::::::::::::::::::::::::::::::
human murine	human murine	human murine	human murine

Fig. 158

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1610		murine ACAAATCTTTTAACCTGAACTCTGGGAAGACTCAAGAGTGGGAGAGAGA	1630 -TAAATTCT	murine CACTGGCTGCTCTTTCAAAGGACCCCAGGTTTGATTCTCAGTACCCACATGGCAGTCCACAGCTCTCTGTA 2010 2020 2030 2040 2050 2060 2060	CCTTC	ACTCCAGACCCAGGGAAATCTGATGCCCTCTCTGGGGGGGCACTGCACAAGCATGGTGCATAGAC 2080 2090 2100 2110 2120 2130 2140	DD	ATATACATGCAAGCAAACGGCTATATATTTTAAAATAAAATGAAAAGTAAAATAATTGAGCCCAATTCTT 2150 2160 2170 2180 2190 2200 2210
	ATAAACCT	rine ACAAATCTTTTAACCTGAACTCTGCC 1940 1950 1960	1620 humanTCTTTAATA	rine CACTGGCTGCTCTTTCAAAGGACCC2 2010 2020 2030	 human	murine ACTCCAGACCCCAGGGAAATCTGATG(2080 2090 2100	human	murine ATATACATGCAAGCAAACGGCTATA: 2150 2160 2170

Fig. 151

Fig. 151

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210	10 210 MKRLLLLFLFFIT	10 LLFLFFITFSS	20 SAFPLVRMTEN	20 30 40 50 60 FSSAFPLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLIDDKIREMQ	40 NQFYSLEIEG	50 NHLVQSKNRSI	60 LIDDKIREMQ
MMP-8	: : : MFSLKTLPI	: ::: :::. MMP-8 MFSLKTLPFLLLLHVQISKAFPV- 10 20	.: :::. ISKAFPVSSK) 20	: ::.:.:: :	···: · · EKFYQLPSNQ 40	YQSTRKNGTNV 50	: .:.::: FRKNGTNVIVEKLKEMQ 60
210 MMP-8		70 FFGLTVTGKLDSNTLEIM :::::::::::	90 100 EIMKTPRCGVPDVGQYGYTL. ::::::::::	ו דק	110 WRKYNLTYRI : . :::::	110 120 130 -PGWRKYNLTYRIÏNYTPDMARAAVDEAIQEG: : : : : : : : : : : : : : : : : : :	130 AVDEAIQEGL .:. :: EVERAIKDAF
	70	80	90	100	110	120 1	130 200
210 MMP-8		LKFTKISKGIA : ::::::: LIFTRISQGEA	GIADIMIAFRTRVHGRCPRY : ::: :: GEADINIAFYQRDHGDNSP- 160 170		LGVLGHAFPP :.:.::: NGILAHAFQP 180	FDGPLGVLGHAFPPGPGLGGDTHFDEDENWT::::::::::::::::::::::::::::::::::::)EDENWTKDG ::.:)AEETWTNTS 200
210	210 210 AGFNLFLVAAHEFGHA:::::::::::	220 AAHEFGHALGL	230 LGLSHSNDQTALMFPNYVS	—	250 YPLSQDDING	250 260 DPRKYPLSQDDINGIQSIYGGLPKV	270 /PAKPKEPTI : .: :
MMP-{	MMP-8 ANYNLFLVAAHEFGH 210 220		LAHSSDPGALI 210	SLGLAHSSDPGALMYPNYAFRETSNYSLPQDDIDGIQAIYG-LSSNPIQPTGPST 210 240 250 260 270	NYSLPQDDID 250	GIQAIYG-LSS 260	SNPIQPTGPST 270

Fig. 15V

210 MMP-8	280 290 PHACDPDLTFDAITTFRR : .::::::::::: PKPCDPSLTFDAITTLRG 280 290	290 DAITTFRREVMI::::::::::	300 340 'RREVMFFKGRHLWRIYYDITDVEFELIASFWPSLPADLQAAYEN-PRDKILVFK :::::::::::::::::::::::::::::::::::	310 YDITDVEFEI :: IPQLQRVEMNI 310	320 IASFWPSLP? :. ::::: ISLFWPSLP?	320 VEFELIASFWPSLPADLQAAYEN-P :::.:::::::: VEMNFISLFWPSLPTGIQAAYEDFD 320 330	340 RDKILVFK :: ::: RDLIFLFK 340
210 MMP-8		350 360 370 380 390 400 410 DENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDAAVCDKTTRKTYFFVGIWCWRFDEMTQTMDKGFPQRV: .:: .:::: .:::: .:::: .::::: GNQYWALSGYDILQGYPKDISNYGFPSSVQAIDAAVFYRSKTYFFVNDQFWRYDNQRQFMEPGYPKSI 350 360 370 380 410	370 380 400 410 PKSIHTLGFPGRVKKIDAAVCDKTTRKTYFFVGIWCWRFDEMTQTMDKGFPQRV ::.: :::: :::: :::: :::: ::::: PKDISNYGFPSSVQAIDAAVFYRSKTYFFVNDQFWRYDNQRQFMEPGYPKSI 370 380 410	380 :DAAVCDKTTF :::: :DAAVFYRS380	390 !KTYFFVGIW(:::::: KTYFFVNDQI 390	400 410 CWRFDEMTQTMDKGFPQ ::.:. :.:.: FWRYDNQRQFMEPGYPK 400 410	410 DKGFPQRV . :.:. EPGYPKSI 410
210 MMP-8		420 430 440 450 460 470 480 VKHFPGISIRVDAAFQYKGFFFFSRGSKQFEYNIKTKNITRIMRTNTWFQCKEPKNSSFGFDINKEKAHS :::: ::::::::::::::::::::::::::::::::	440 FFSRGSKQFEN : HVFSGPRYYAI 440	0 450 460 GSKQFEYNIKTKNITRIMRTNTWFQCK :::::::::::::::::::::::::::::::	460 IMRTINTWFQCI : : : ARGNKWLNCI 460	470 KEPKNSSFGFD ?	480 INKEKAHS
210 MMP-8		490 500 510 GGIKILYHKSLSLFIFGIVHLLKNTSIYQ :	510 LKNTSIYQ : :				

Fig. 15W

ngymana at tron

Fig. 15X-1

ngykanan na kana

210 MMP-8	280 330 310 320 330 330 330 330 330 330 330 330 340 34	290 'GA-TGTGG-G(::.:::: 'GACAGTGGTG(300 CCAGTATGGC' . ::: GTTTTATGTT	00 GCTACACCC .:: :: TTAACCCCAGG?	310 TCCCTGGGT .::: .:: AACCCCAAGT	320 TCCCTGGGTGGAGAAATAC .::::: ACCCCAAGTGGGAACGCACT 320 330	330 CAACCTCA :::::: TAACTTGA 340
210 MMP-8	340 350 400 CCTACAGAATAATAAACTATACTCCGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTT :::::::::::::::::::::::::::::	350 TAAACTATAC' :::::::: :GAAACTATAC' 360	360 TCCGGATATG ::.:::: CCCACAGCTG	370 GCACGAGCTG ::::: TCAGAGGCTG	380 SCTGTGGATGA ::.::.:	360 370 380 400 CTATACTCCGGATATGGCACGAGCTGTGGATGAGGCTATCCAAGAAGGTTT :::::::::::::::::::::::::::::	400 GAAGGTTT ::.: :: GATGCCTT 410
210 MMP-8	410 420 430 440 450 460 470 210 AGAAGTGTGGAGCAAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATT .:::::::::::::::::::::::::::::::::::	420 CAAAGTCACT : .:. TGTTGCATCA(430 CCACTAAAAI ::.::::: CCTCTCATCI	440 TCACCAAGAT ::::::::::::::::::::::::::::::::::	450 TTCAAAGGGG ::::::::	430 440 450 460 470 ACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATG .:.::::::::::::::::::::::::::::::::::	470 TCATGATT :::.:: TCAACATT 480
210 MMP-8	480 GCCTTTAGGAC :: :: GCTTTTTACCA 490	490 TCGAGTCCATG . ::. :: : AAGAGATCACG) 500 510 STCCATGGTCGGTGTCCTCGCT :. :: :: :: :: :: :: :: :: :: :: ::	510 TCGCTATTTTG:::::::::::::::::::::::::::::	520 GATGGTCCCTT(::::::::::: GATGGACCCAA') 520 540 STCCATGGTCGGTGTCCTCGCTATTTTGATGGTCCCTTGGGAGTGCTTGGCCATG . :: :: :: :: :: :: :: :: :: :: ::	540 TGGCCATG :: ::: TGCTCATG 0

Fig. 15X-2

210 MMP-8	550 560 CCTTTCCTCCTGGTCC ::::: ::::: : CCTTTCAGCCAGGCCA	550 560 610 210 CCTTTCCTCCTGGTCCGGGTCTGGGTGACACTCATTTTGATGAGGATGAAACTGGACCAAGGATGG :::::::::::::::::::::::::::::::	570 580 590 GGGTCTGGGTGGTGACACTCATTTTGATGAG .::::::::::::::::::::::::::::::::::::	580 ACACTCATTTT : .:::::: ATGCTCATTTT 580	590 TGATGAGGATG :::: :::: TGATGCCGAAG 590	570 580 590 600 610 GGGTCTGGGTGACCACTCATTTTGATGAGGATGAAACTGGACCAAGGATGG .:::::::::::::::::::::::::::::::::::	610 .ccaaggargg :::: . .ccaacaccrc 610
210 MMP-8	620 630 AGCAGGATTCAACTTG :::::::: CGCAAATTACAACTTG 620 630		640 TTGTGGCTGCTC :::::::: TTGTTGCTGCTC 640	650 :TCATGAATTTG ::::::::::::::::::::::::::::::	660 GGTCATGCACT ::::::: GGCCATTCTTT 660	640 650 660 670 680 TTTCTTGTGGCTCTCATGAATTTGGTCATGCACTGGGGCTCTCTCACTCCAAT ::::::::::::::::::::::::	680 TCACTCCAAT ::::::::: TCACTCCTCT 680
210 MMP-8	690 700 210 GATCAAACAGCCTTGA ::::::::: MMP-8 GACCCTGGTGCCTTGA 690 700	700 GCTTGATGTTC GCTTGATGTAT 700	710 CCCAAATTATG1 :: :::: TCCCAACTATGC	720 GTCTCCCTGGA : : : :: GCTTTCAGGGA 720	730 ATCCCAGAAAA :. ::: :: AAACCAGCAAC	710 720 730 740 750 TGTTCCCAAATTATGTCTCCCTGGATCCCAGAAATACCCACTTTCTCAGGATG :::. :: :: :: :: :: :: :: :: :: :: :: ::	750 TCTCAGGATG ::::::::::: :CCTCAAGATG
210 MMP-8	760 770 210 ATATCAATGGAATCCA :::::::::::::: MMP-8 ACATCGATGGCATTCA 760 770	770 SAATCCAGTCCA': ::: SCATTCAGGCCA'	780 GTCCATCTATGGAGG1 : ::::::::: GGCCATCTATGGA	790 800 TCTGCCTAAGGTACCTG(:: ::: .::CTTTCAAGCAACCCTA' 790 800	800 GTACCTGCT? ::. AACCCTATCC 800	780 810 820 GTCCATCTATGGAGGTCTGCTAAGGCCAAAGGAACCCACTAT : ::::::::::::::::::::::::::::::::::	820 ACCCACTAT :::::: ACCAAGCAC 820

Fig. 15X-3

830 840 850 ACCCCATGCCTGACCTTGAC :::::::::::::::::::::::::::::::::::	830 850 890 890 890 890 890 890 890 890 800 80	900 910 920 930 940 950 960 210 AAAGGCAGCTATGAGAT-CTATTATGATATCACGATGTTGAGTTTGAATTAATTGCTTCATTC :::::::::::::::::::::::::::::::	970 980 1000 1000 1010 1020 1030 TGGCCATCTCTGCCAGCTGCATACGAGAACCCCAGAGATACTGGTTTTTA ::::::::::::::::::::::::::::::	1040 1050 1060 1070 1080 1090 210 AAGATGAAAACTTCTGGATGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATC-CATACAT :::::::::::::::::::::::::::::::::::
	830 840 850 CCCATGCCTGTGACCTTGAC ::::::::::::::::::::::::::::::::::::	900 910 920 AGGCAGCCTATGGAGGAT-CTAT :::::::::::::::::: AGACAGGTACTTCTGGAGAAGGCAT(900 910 920	970 980 990 GCCATCTCTCCCAGCTGATCTGCAA(:::::::::::::::::::::::::::::::::::	1040 1050 1 AGATGAAACTTCTGGATGATCAGAG ::.::::::::::::::::::::::::::::::::

Fig. 15X-4

L : L	4 . 5 5 . 5	L1 -	₹ ₹
40 1150 1160 TCTGTGATAAGACCACAAGAAAACCTACTT :::::::::::::::::::::::::::::::::::	10 1220 1230 CCAAACCATGGACAAAGGATTCCCGCAGAGA :::::::::::: AACCAAAGACAATTCATGGAGC 1200 1210	TCTT	AACTZ
50 AAAAC ::::: AAAAC 1160	30 FCCCG :CA)0 ATTCT : : .	70 ATGAG
1160 AAGAAA :::::: AAGTAA	1230 GGATTC	1300 AAGGAT ::: AGAGAG 0	1370 CGAATCAT .:: TTC
0 ACCAC : :: TACAG 1150) ACAAA ACAAT 1210) GTACAA : : : : GGAATA 1260) ACCCG .: .: .13
1150 TAAGA : TTTCT	1220 AACCATGGACAAA ::::::::::: AACCAAAGACAAT 200	1290 1300 CTTTCCAGTACAAAGGATTCTT :::::::::::::::::::::::::::::::::	1360 AGAATATTAC :::::::: AGAACATTTC
0 CTGTGA ::. TGT 1140	AAACC :::: -AACC 1200		50 1360 137 CAAAGAATATTACCCGAATCA ::::::::::::::::::::::::::::::::::
⊢ (') 1	1210 ACCC?	1280 1290 1300 GTTGATGCTGCTTTCCAGTACAAGGATTCTTC .:.::::::::::::::::::::::::::::::	1350 GACAAA(: A
SCAGC	AAATG	TGTTG .: AG	ATTAA : }
1120 1130 CGTGAAGAAATAGATGCAGC :: :.: :::::::::::::::::::::::::::::::	1200 'TGATG2 :::: 'TGAT	1270 ATCCG7 ::: ATC	1330 1340 AAGCAATTTGAATACAACAT :::::::::::::::::::::::::::::
1 AAAAT :::: 3CAAT 1130	0 1180 1190 1200 CTTTGTGGCATTTGGTGCTGGAGGTTTGATG.::::::::::::::::::::::::::	0 1260 1270 ACTTTCCTGGAATCAGTATCCG' :.:::::::::::: TATCCCAAAAGCA-TATC 1230 1240	3AATA : : TC
1120 GTGAAG :: :. GTCCAA(1190 GCTGGAG :::::: TCTGGAG	1260 TGGAAT(:: CAAAAG(0	1330 3CAATTT(:::.:: 3CAGTTT- 1280
11 .CGTGT : :: ?AGCGT	11 3GTGC ::	12 TCCTG ::: . TCCCA	1330 AAGCAAT ::::: GCAGT 1280
O 'AGGA(':	.0 'GACC' 1180	.ACTTTC : TATC	.0 !ATCA! ::
1110 TAGGTTTTCCAGGA .::::::::	1180 rgggca' : raaarg	1250 AAAACA(1320 AGCCGTGGATC ::::: GTTGAT- 1270
AGGT.	0 CTTTGTGGGC ::::: CTTTGTAAA1	TGGT7	0 TCAGCCG; : G; 1270
1100 1110 1120 1130 1140 1150 1160 210 TAGGTTTTCCAGGACGTGTGAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAACCTACTT::::::::::::::::::::::::::::::::::	1170 1180 1190 1200 1210 1220 1230 210 CTTTGTGGGCATTTGGAGGTTTGATGAATGACCCAAACCATGGACAAAGGATTCCCGCAGAGA :::::::::::::::::::::::::	1240 1250 1260 1270 1280 1290 1300 210 GTGGTAAAACACTTTCCTGGAATCAGTATCCGTGTTTGATGCTGCTTTCCAGTACAAAGGATTCTTTTT .::::::::::::::::::::::::::::::	1310 1320 1330 1340 1350 1360 1370 210 TCAGCCGTGGATCAAGCAATTTTGAATACCAACATTAAGACAAAGAATATTACCCGAATCATGAGAACTAA :::::::::::::::::::::::::::::::::
, MMI	, ММ	, MM	, MMI

Fig. 15X-5

ngy na maranan

1380 1490 1410 1420 1430 1440 210 TACTTGGTTTCAATGCAAAGAACTCCTCATTTTGGTTTTTGATATCAACAAGGAAAAGCACAT ::::::::::::::::::::::::::::::::::	1450 1460 1470 1480 1490 1500 1510 210 TCAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCTTGTTTTTTTGGTATTGTTCATTTGCTGA :::. ::. ::.:: ::.:: ::.::::::::::::::	
0 1390 1400 1410 1420 1430 1440 TACTTGGTTTCAATGCAAAGAACTCCTCATTTGGTTTTGATATCAACAAGGAAAAGCA(A) ::::::::::::::::::::::::::::::::::	1490 . 1500 TAAGCTTGTTTATTTTTGGTA: ::::GCAATAAATGG	
1420 TCATTTGGTTT:::::::::::::::::::::::::::::	1490 · TAAGCTTGT' ::GCA	
1410 AAAGAACTCCT ::: : : AAGATATTACG	470 1480 TTGTATCATAAGAGTT ::.:::: GTTGCAAGAG	
1400 CAAAGAACCA ::::::: CAGTGGACCA 1320	1470 ATATTGTAT(::. GTTG('ATCAA . : 'GGC
1390 GGTTTCAATG : :: : GTCTT	1460 AGGCATAAAG	1520 1530 210 AAAACACTTCTATTTATC :.: ::: :
1380 210 TACTTG :::: MMP-8CATG	1450 210 TCAGGA :::. MMP-8 -CAGA- 1360	1520 210 AAAACA :.: MMP-8 AGA

Fig. 15X-6

139 38 199 259 319 98 439 18 58 379 118 138 499 AGC L AGC GAAAAGCGCTGGCCCGGGCCCCGCCGCCCGCCCGCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAAGGCTTCCAGCC TTGAAT CTT Ц 口 ഗ ഗ z CGG TIC ACC GTG CAC PCCT AAC > 出 ACC E z ഥ ₽ AGC I ATC TCG CIC S AGC GIG Ы > ß ACA ഗ ⊱ GAC P GAG CIG CTC GAC CAG Ы ы Ω Ω [T] Ø TIC GTG AAT AAC GAC AGC Д GCC > ß z ഥ Z CCG GTG CAC CIG CTT LCTT Ы GGG Ы Д > 田 ᠐ GGC ATG ATG S AGC S TCG CCC Д Ö Σ AGT Σ വ TIC I ATC GAG CIC TCA E GAG Ы വ GTG 闰 ſΞι ACC CAC GAT AGC CTG L Ы Д ß GCC Н 耳 ď GAG ACC Γ Y TAC CCC CGG Н CTG 口 Д ద Ц GTG AAC GGC TIC GGC R GGC CTG > ט Ŋ ഥ Z Ы GAG TCC A GCT AGC CTG LCTT CIG Ы ß ഥ വ Ы GAG JGC GGC ICC Γ R CGC Ö 臼 CTG ტ ഗ Ы T ACG ICC GCC CAA AGC CIG 니 വ ø CTG Ø ഗ Ц TACG TGC GAC TTC TGT CCA Д U Ö ഥ CCC Ω Д GGG TAC GCC CTG GAT TIG П Ц \succ ø Ц TGG Ç ⋈ ggG GCC CCC CAC TACT GTG Ŋ ď Д > CCG 耳 Д TIC CGG CCC CCG PCCC ACA Ø Н ATG Д α Ŀ Σ IGC CIG T ACT ACA GGG TCA Ç വ Ы CCCACC Ö 더 GCG ATC GGC L GAC CCA ď Ŋ Д Ω Н

Fig. 16A

198 679 178 619 218 238 258 859 278 919 S AGC R CGG R AGG A GCC A GCT V GTC L CTG Ы д 36С T ACG H L A GCC A GCG Q CAG G G G G Q CAG P L L P L E GAG S ICA H N AAC S AGT R CGG S TCT G GGC FITT P CCT N AAC H CAC P GGG L CTG P V GTG L TACG W TGG D GAT H V GTG L E P T ACG L A GCC L T ACA E GAG A GCT V GTG F ITC R Γ S AGC L R GGA L A GCC H N AAC L CTG G GGC FTTC A GCA N AAC Y TAC I ATT L GGA G GGC TACC S TCT W TGG LCTC V GTG S AGC R L N AAC G G G S AGT N AAC Q CAG S TCA L G GGG P S TCG L V H I ATT P A GCG A GCG K AAG CHT E GAG S TCC TACC D GAC L F r GIG P A GCC L P DGAC N AAC R GGG EGAG L L DGAC A GCG R CGA GGT PCCT G G G EGAG Q V GTG P L P L S Q CAG N AAC H L N AAC G GGT R AGG L L GGC P D S TCC H L I ATT Q CAG A GCC V GTC SAGC V GTG L L S AGC A GCA

Fig. 16E

318	1039	338	1099	354	1147
	CGC		CAC		
ద	CGG	Ы	CTG		
บ	TGC	Ø	೦೦೮		
ద	CGG	>	GTG		
>	GTG	¥	AAG	*	TGA
Д	GAT	Д	CCC	Н	$_{ m TTG}$
Ø	CAG	ഗ	AGC	н	ATC
ტ	GGC	ഗ	ICC	₽	ACC
>	GTG	Ü	GGC	Д	CCC
യ	AGC	വ	CCT	ט	GGC
	GTC	ద	AGG	ద	AGG
ഗ	AGC		CGG	Ø	300
Q	CAG	<u>ப</u>	CCC	Ø	GCT
Н	CIG	×	TAC		$_{\mathrm{ICI}}$
Ą	GCA	⊣	ACC	田	GAA
Д	CCG	ტ	299	ഷ	CGG
Ц	CIC	ы	GAG	Н	ACC
Ħ	CAC	ద	CGG	Ω	GAC
Ы	CIC	>	GTG	>	GTA
	CIC	П	CIG	บ	TGC

1779 2016 2095 1463 1542 1700 1621 ACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGAGTTCAGGTCCACTGGGCTGAGTGTCCCCTTGG CCTTGCCTGTTCCCCATTAGCACAGGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTG CAAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCCTGGGCTGCCTCAGGTCCCGAGTAACTTATGTTCAATGTG CCAACACACGGGGGGGGGCCCGCAGGCCTATGTGGCAGCGTCACCACAGGAGTTGTGGGGCCTAGGAGGCTTTGGACCT GGGAGCCACACCTAGGAGCAAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGACTTCGATGC CATCCTTTTCTATTTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAAATCAAGTCCACCCTTCTCATGTGACAGAT SCCTCCCAGCCCGGACCCAATGCACTTTCTTGTCTCTCTTAATAAGCCCCACCTCCCCGCCTGGGCTCCCCTTGCTGC ACCAGCTGTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTTCCAGCCTAGC CAGITICICACCCIGGGIIGGGGICCCCCAGCAICCAGACIGGAAACCIACCCAITITICCCCTGAGCAICCIAGAIG GGCCCTGAGCACGACAGCCCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCATGTCTATG

Fig. 160

DOFESTED OS SOS

2490 2569 2628 2411 CACATGGGCATCAGGGGCTGGCCCCACAGAGACCCCACAGGGCAGTGAGCTCTGTCTTCCCCCACCTGCCTAGCCCATC CTCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCCTGGGCTGTTTCCTTAGTCTTCATTTATAAAAGTTGCTTT TTTAACGGAGTGTCACTTTCAACCGGCCTCCCCTACCCCTGCTGGCCGGGGATGGAGACATGTCATTTGTAAAAGCAGA AAAAGGTTGCATTTGTTCACTTTTGTAATATTGTCCTGGGCCTGTTGGGGGTGTTGGGGGAAGCTGGGGCATCAGTGGC

Fig. 16I

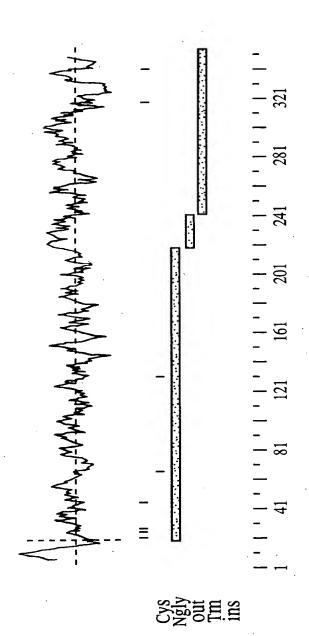


FIG. 16E

79 15 23 31	37	r
CCTC SAAT SCAA	M L I G E I F E L M Q F L F V V A F T 1	D Y D I L F A N K M V N H 3
GAGG	F	Z
GTCGACCCACGCGTCCGCCCGGCCTAGCGCCCGCGGGTCGCCCGAGCCGAGCCGAGCCGAGCCGGGGGGGG	A GCC	>
ABGCC CAGTT	V GTT	Σ
GCGC GCGC ACGT	V GTG	×
CCGA CATG CTGC	F TTT	Z
CGAG TGGT GTTG	L	Ą
GAGG GCGG ACCT	F	দ
AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Q CAG	ᆸ
GCCC GACA GGAG	M ATG	H
TCGC GGTG CAGG	L	Q
CGGG TCAA CCCC	E	Ħ
GCCG GTGG TTCA	F TTT	Д
TAGC	I ATC	
GGCC TTCC TATA	E	บ
GCCC GCTG CTCC	GGG	ഗ
GTCC GGTC AGGC	I ATC	>
ACGC CCCG CTAG	L	ᄓ
ATCA GCGC	M ATG	T F L V S C V
GTCGACCCACGCGTCCGCCCGGCCTAGCGCCCGCGGGTCGCCCGAGCCGAGCCGAGCCGAGCCGGGGGGGG	TGT	⊢

8 7 9

9 0

99 I ATC E GAG $\overline{\mathbf{W}}$ $_{\rm TAC}^{\rm Y}$ C TGC C TGC I ATT N AAC Y TAT I ATC F TTC K AAG I ATC LCTT R CGG H I ATC W TGG F TTC V GTC

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79 556

G GGT

A GCT

I ATT

V GTC

L CTG

I ATC

TACC

I ATC

LCTT

S TCC

g GGC

N AAT

E GAA

Q CAG

I ATT

R AGG

A GCC

S AGT

 $_{\rm TGT}^{\rm C}$

V GTC

59 496

o CAA

A GCT

PCCT

 $\frac{1}{1}$

F TTT

A GCC

D GAC

PCCA

L

TACT

V GTC

K AAG

V GTC

PCCC

E

TACT

PCCT

H CAC

L CTT

S AGT

436

CAC

AAC

GTG

ATG

AAG

AAC

GCC

TTT

CTA

ATC

GAC

TAT

GAC

GIG

IGC

AGC

GIC

CIG

TTC

ACC

119 676 W TGG TACG C TGC Y TAT P LCTT A GCC S TCT ATG Σ PCCT I ATC R Γ A GCT H Γ Y TAC F TTC S TCC H

Fig. 17A

.4

239 259 1096 179 856 199 916 219 V GTG 0 0 0 0 0 K AAA A GCT L CTA Γ Γ CAC M ATG E PCCT R CGG L V GTG 出 I ATC Y TAC GGG GGA O CAA E GAG F TTC r C TGC N AAC L W TGG G GGG N AAC A GCT I ATC Q CAG ი მმ*ც* GGC $_{
m F}$ Y TAT A GCT Q CAG L I ATC FTTC R CGT S AGC PCCT I ATC H L ာ ၁၅၅ K AAA F R CGT E GAG R GGC L Y TAC F L I ATT K AAG I ATC F E GAG E GAG W TGG A GCC Q CAG R A GCC L CTG R GGC FTTT Y TAT T ACG N AAC K AAG I ATC L L H Q CAG Y TAC I ATC Y R CGC PCCT L K AAG V GTG I ATC Γ S AGC N AAC Q CAA LCIC I ATC D GAC L W TGG S AGC W TGG R CGG L S GGT L E I ATA A GCC K AAA R r GGC E GAA CGT N AAT ద Q CAG N AAC TACC Q CAG L I ATC T ACA TTC V 3TG L A GCC CIC V GTT FITT 压 E GAG L CTG F L L CTG P CCC E GTC E C A GCA Q CAA R S TCT >

Fig. 17B

279

LCTC

Y TAC

C TGC

R

G GGC

Y TAT

L

S TCA

C TGC

R

A GCA

.G GGA

L

A GCC

. GGG

P

E GAG

R CGG

K AAG

W TGG

1336 379 1516 PCCC G GGA GAT GTG V GTG Q CAG > Ω K AAG N AAT E GAA T R GGC S TCG Y TAC K AAG D GAC GTG LCTC R CGC > A GCC g GGC Y TAT TACC L CTG H V GTC L CTG I ATT Q CAG A GCC R CGT TACC N AAC LCTG GGG E GAG N AAT L CIC Γ G GGT T ACA P CCT A GCC R CGC L ITG Γ C TGC Q CAG I ATT TACA F S L W TGG Q CAG LCTT V GTC V GTG H CAC P CCT T D GAC L V GTG M ATG S TCA TACC E GAG $\frac{L}{\Gamma TG}$ A GCT H P CCT Γ CAC F L Q CAG M ATG E GAG I ATC V GTG D GAC Y TAC C TGC S H CAC L N AAT H P E M ATG а 960 E GAA I ATC I ATC Y TAC V GTG H N AAC A GCT F TTT F K AAG F S TCC A GCT A GCT R AGG F L ITG L CTC H S TCC CA GCC A GCC V GTG I ATC

Fig. 170

GAG

团

L

A GCC

R CGG

P CCA

R CGC

L CTG

C TGC

 $_{
m F}$

I ATC

L

I ATC

LCTC

P

T ACA

V GTC

I ATT

P

S AGC

Ы

CTG

 $\frac{L}{TTG}$

E

E

 $\frac{1}{1}$

I ATT

F

V GTG

A GCA

K AAG

Y TAC

Q CAG

 $^{
m F}$

L

Q CAG

A GCC

FTT

E GAG

D GAC

R CGG

TACC

CHT

S AGC

L

P

E GAG

S TCT

E GAG

S TCT

o Caa

L TTA

S TCC

Q CAG

I ATC

S TCT

T ACG

FTT

L

A GCC

N AAT

闰

GAA

499 1816 479 1756 S TCC T ACA FTTT Q CAG CAC C TGC 田 TACC M ATG G GGG D GAT L A GCT GGA S TCA S TCT V GTG L L ITG GGT W TGG E TACA V GTT Q CAG V GTC K AAG P CCC GGA E H ט V GTG D GAT GGT TACC E H CAT F TTC Q CAG A GCT N AAC Q CAA R CGC Q CAG R CGA V GTT Y TAC F D GAT M ATG V GTG F TTC DGAC Q CAG S TCA A GCC I ATA A GCT E GAG F TTT

519 1876 539 1936 LCTC PCCT F LCTC G GGC L L GGT FTTC G GGG A GCC Q CAA ACA A GCC \vdash S AGC LCTC E GAG S AGC A GCT R CGT P CCA A GCT P A GCA Q CAG G GGA D GAT W TGG G GGC R CGG PCCT Q CAG N AAC V GTT TACC Q CAG I ATC E GAG BCC K AAG Ø

579 2056 Q CAG L D GAC R AGA P L PCCA PCCT G GGC R CGG C TGC S TCC S TCA а 960 A GCT V GTA V GTG N AAT A GCA I ATC

P Q CAA Γ P S F S TCC R CGC Γ A GCC S TCT A GCC V GTC E A GCT R AGG H R AGG S TCC а 960

Fig. 17D

2356 669 2416 639 629 619 619 719 CAG GAA ი მმ*ი* R AGG E GAA GCT CAT PCCT Ø 闰 Ø 王 A GCC Q CAG S TCA GGA S TCT ი მმ H S TCT Ŋ K AAG R AGG GAT AGT R CGC H CAT P L CTG О ഗ V GTG V GTG H E GAG PCCT LCTG TCA V GTT ß GGG L CTG L D GAT I ATC A GCC GCA R AGG Ö Ø Q CAG S AGT TACC P S TCG S TCT S AGC S TCT а 960 H CAC E GAG Q CAG T ACC Q CAG Q CAG V GTG T ACA L M ATG R PCCC E GAG TACA G GGG M ATG G GGC Q CAG Y TAT R A GCC PCCT D GAT TACC L H P CCT E GAA GGA R CGG A GCT A GCC GCA S AGC W TGG A GCC G GGA D GAT E GAA Ø H CAC H CAT V GTA g ggc T ACA W TGG W TGG PCCT A GCT V GTG L H CAT E GAG R CGG I ATC ი მმმ S AGC R CGG GGA P GGC GGA R GGG S AGC M ATG E GAG G GGG а 660 S AGC A GCA GGT L TAC G GGG E GAG E A GCA T ACA PCCT P CCT × R CGC $_{
m CTG}$ P S TCC T ACA E GAA D GAT C TGT S AGC S TCC A GCT PCCC R CGG PCCT R AGG Q CAG Q CAG A GCC A GCC A GCA Y TAT Q CAG S TCT A GCC Y TAT S AGC S AGC F T ACA ſщ

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17E Fig.

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у т т т т т т т т т т т т т т т т т т т	2656	2735	2814	2893	2972	3051	3130	3209	3288	3367	3446	3525	3604	3683	3762	3770
ĸ	TCG GAG GAT GAG CTA CCC CCT CAG GTG CAC AAG GTA TAG	ACGG	GTGTGGTGTTTGTGTGTCTGTGCCTGGCCAAGGGAGGTGCCAACACTGGGC	ממכמ	TIGGCTCAGAGIGIGGIGCTAGAAACTGGICCCCAGCCCAG	IGGA	BLIC	FTCT	CTAT	AGGA	TGGGCCCCCAGGAGACTGAGGTCTTCCTGGGCCCTCATTGCTGCTTATCGTACCCCCCATCACCTGCACATGGGACAGA	3666	CCCT	GTGT	AAGG	
>	GTA	rggg	CACT	3GAC	rgca	BGCC	CGCA(CCTG	4ACG	LTTT.	3GGA	3AAG	CCAC	3ACC(AAAA	
4	AAG	3CCA.	CCAA(CCCA	ממכנו	3TTG	CACC	rgcT(CLLC	CATC	ACAT(CCL	rgtc(ragg(AAAA	
ヸ	CAC	3CCT(3GTG(CATC	CCTA(3GAG(ACCT(rgcT.	CICC(LTGC	CTGC	rgTG(rctc.	\GGG.	AAAA	
>	GTG	3TCT(3GGA(3CCT(raca(3TGG(CTTZ	3TGC.	CAG	3CCC.	CAC	raga:	CTAC	3AGC2	JAAA	
אכ	CAG	וככככ	CCAAC	rcta(CCTT	rgga(rgga	TCTCCGCTTCTTGCACATCACTGGCCTGTGTGTGCTGCTTGCT	TTGCTTTGCGTTAGGGTGAAGACCCTAGCGTCCAGCTCCCCTCAACGCTAT	rgCT(CCCA	'ACGTCCCAGCAAAAGAGCTCTGGCCCGCATCTCGCTGTGCCCTGAAGGGGG	'TGGGCTGCTGCACTGCATGCTGGGACTGCTCCTACTCTGTCCCACCCCT	GTGGTGAATTGCGCTGCCCGAACTCGGAGCGGAGCAGGGTAGGGACCGTGT	AAAA	
Ъ,	CCI	3CCA.	CTGG(3GAC.	3CCA(ACTG.	3CTG.	CCT	CCTA	ACTT.	ACCC	CCCG	3ACT(rcgg7	LAAA	
ንነ	CCC	CCT	3TGC(CACG	PACT(3CCA1	rcag(ACTG	4GAC(AAAT?	rcg _T	CTGG(CTGG	3AAC.	AAAA!	
7	CTA	3CTG(3TCT(3GCA(CAG.	TGT(ZAGG.	CATC	3TGA1	\TGG1	CTTA	AGCT(CATG	3000	JAAA	
괴	GAG	CACC	FIGT(CGAG	4GCC(BAAC	rgag(rgca(ragg(CAGG2	3CIG(AAAG1	\CTG(CGCT	LAAA	
⊐	GAT	\GGC(FTTT(BAAC	3000	3GGA(raga.	lTCT.	3CGT.	3GAG(CATT	AGCA1	TGC	\TTG	CAG	
r]	GAG	TGGZ	GGT(TAG	CCAC	4GCAC	CAA7	CGGC	TTT(rgTA(CCL	נכככז	CTG	TGA	LTGA(
ע	TCG	AGGZ	'GTG	BGGCC	GICC	CCA	מממ	TCT	TTG	AAATT	השפה.	TACGI	TGGC	\GTG(AGT	
•	GGC	BGCCC	ACGI	TIGG	ACTO	GCTG	AGCC	CCTC	GCTJ	TCL	ביביביי	GTG	3GCTJ	GAG2	AGGG	
괴	GAG	TGT	SCCC	GAAT	'AGA	AGAZ	נטטטנ	CTCZ	TICC	\GGT]	GTCI	בישפים.	CGAG	TTG	AAA.	
긔	GAA	TTCC	CTGG	AGAG	TGCI	CGAI	CCTI	CCGG	TCCG	AGAZ	TGAG	CCLI	נפככ	GGCI	TAAT	
٦,	CCC	AGGG	TICC	CAGG	GTG	CCCZ	GCA2	GCAG	CCGI	AAAA	AGAC	GTG2	בטטפי:	GICC	CCCI	
고 고 고	GAG CCC GTG CCC GAA GAG GGC	<u> ACAAGGCTGAGCAGGGTTCCTGTGGCCCCAGGATGGAGGCCACCGCTGCCCTGCCATCCCGTCTGCCTGC</u>	CTCCTCTGAGTGTTCCCTGGCCCCCACGT	TTGCCACAGGCCCCCAGGAGGAATTTGGGGCCTAGGAACCGAGGGCACACGGGGACTCTAGCCTCATCCCCAGGACCCCC	GAG	CCCAGAGGGCTGCCCACGATAGAAGCTGCCAAGCAGGAGAACCTGTGCCAACTGTGGAGTGGGGAGGTTGGGCCTGGA	CCCTCAACCCCTGCAACCTTCCCTAGCCCCCTCAATAGATGAGCAGGTCAGGCTGTGGCCCTTACCTCACCCGCAGTTC	TCGCCCAGTGCTGCAGCCGGCTCACCTC	GTTCGCTTGCTCCCGTTCCGTTCGGCTT	ATTITGACACTAAAAAAAGAAGGTTTCTAAATTGTAGGAGCAGGATGGAAATACTTTGCTGCCCTTGCCATCTTTAGGA	CAGG	CCGGGCTGGAGGGTGACCTTGGCTGTGT	ATGAAGGGCGATGCCTCGCCCGAGGCTT	CACCCAGCTGTGGTCCGGCTTTGGGAGA	ACAGCTTGATAAAAAAAAAAAAGGGAGTTTGACCAGAAAAAAAA	r
Э,	ααα	GGCT	TCTG	CACA	CTCA	GAGG	CAAC	CCAG	GCTT	TGAC	CCCC	GCTG	AGGG	CAGC	CTTG	しせししせせしせ
ī	GAG	ACAA	CTCC	TTGC	TTGG	CCCA	CCCI	TCGC	GTTC	ATTI	TGGG	CCGG	ATGA	CACC	ACAG	C C C C

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Fig. 171

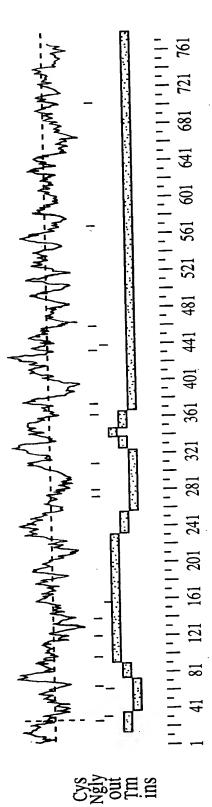


FIG. 176

79	9	29	49	69 326	88 386	109 446	129 506
STCG	<i>(</i> h	V GTC	R CGA	EGAG	Y TAT	K AAG	N AAT
CGGG	O CAG	CAC	S TCT	FTT	D GAC	V GTC	E GAA
CACC	Y A TAC	V GTG	F TTC	I ATC	V GTG	P CCC	Q CAG
GAAJ	E GAA	$_{ m TTG}$	F TTC	E GAG	C TGC	E GAA	I ATT
TCT	T : ACT	$_{ m CTG}$	CIC	GGG	S AGC	T ACT	R AGG
BAGCC	D CAC	D GAC	D GAC	I ATC	V GTC	PCCT	A. GCC
99299	F TTT	E GAG	CTT	CIC	L	H CAC	S AGT
BCCG	Q ; CAG	E GAG	N AAC	M ATG	F TTC	L	C TGT
;cgg⁄²	A GCG	G GGG	E GAA	C TGT	T ACC	S AGT	V GTC
CGAG	M 3 ATG	P CCA	I ATT	T ACA	T ACT	H CAC	O CAA
GAGO	GGTG	P CCC	H CAT	F	F TIC	N AAC	A GCT
AGCC	30661	S TCA	H CAC	9 9	A GCC	V GTG	P CCT
PGCCG	99999	D GAT	W TGG	N AAT	V GTT	M ATG	Γ
3CCG?	acae	S D AGT GAT	P CCT	K AAG	V GTG	K AAG	${ m F}$
າດອີດ	GTGG	Y TAT	S TCA	Q CAG	F TTT	N AAC	A GCC
36651	CAAG	S TCC	K AAG	H CAC	L	A GCC	D GAC
9503	TGGI	A GCC	S AGC	CTG	F TTC	FTT	P CCA
AGCG	GAGG	E GAG	999	N AAT	Q CAG	L CTA	L CTG
CCCGGCCTAGCGCCGCGGGTCGCCGAGCCGAGCCGAGCC	CTGTTCCTGAGGTGGTCAAGGTGGACAGGGGGGGGGGTGGTG	L CTA	E GAG	Y TAT	M ATG	I ATC	T ACT
ອນນ	CTGI	R GGC	A GCC	V GTT	CTC	D GAC	V GTC

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Fig. 17E

corena en a mana

				170/361			
149 566	169 626	189 686	209	229 806	249	269 926	289 986
K AAG	R CGC	Q CAG	Y TAC	CCT	Y TAC	L	CGC
I	L	V	I	$_{ m CTG}$	K	S	N
ATC	CTG	GTG	ATC		AAG	AGC	AAC
L	A GCT	I ATC	D GAC	L	L	W TGG	S AGC
R CGG	H CAC	R.	$_{ m CTG}$	S TCC	G GGT	E. GAA	L
H	L	A	E	K	R	N	R
CAC	CIG	GCC	GAA	AAA	CGT	AAT	GGC
I	Y	Q	T	N	T	L	Q
ATC	TAC	CAG	ACA	AAC	ACC		CAG
W	F	V GTG	L CTG	V GTT	F TTC	F TTT	A GCC
TIC	S	E Gaa	E GAG	L CIG	F TTC	CIG	L CTG
V	H	Q	R	A	V	S	EGAG
GTC	CAC	CAA	CGT	GCA	GTC	TCT	
GGT	I	W	K	V	A	355	L
	ATC	TGG	AAA	GTG	GCT	GGC	CTA
A	E	T	H	M	E	PCCT	R
GCT	GAG	ACG	CAC	ATG	GAA		CGG
I	W	C	I	Y		G	Q
ATT	TGG	Hec	ATC	TAC	GGG	GGA	CAA
V	Y	Y	C	N	CIC	W	G
GTC	TAC	TAT	TGC	AAC		TGG	GGG
L CTG	C TGC	P	I ATC	Q CAG	GGC	F TTC	
I ATC	C TGC	CIT	Q CAG	F TTC	P CCT	L	R CGT
TACC	I	A	H	R	L	I	K
	ATT	GCC	CAC	CGT	CIG	ATC	AAA
I	N	S	E	L	R	L	Y
ATC	AAC	TCT	GAG		CGC	CTG	TAC
L	Y	M	K	I	F	E	E
	TAT	ATG	AAG	ATC	TTC	GAG	GAG
S	I	P	Q	R	CGC	F	A
TCC	ATC	CCT	CAG	CGC		TTT	GCC
9 9	TIC	I ATC	T ACG	H CAC	L	N AAC	K AAG

Fig. 17]

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309	329	349	369	389	409	429	449
1046	1106	1166	1226	1286	1346	1406	1466
I	A	E	$_{ m ITG}$	A	T	H	P
ATC	GCA	GAG		GCT	ACC	CAC	CCT
O	G	. H	F	L	$_{ m CTG}$	Q	M
CAA	GGA	CAC	TTC	CTG		CAG	ATG
W	L	E	C	I	V	D	Y
TGG	CTG	GAG	TGC	ATC	GTG	GAC	TAC
I	A	L	N	S	H	P	H
ATA	GCC	CTG	AAT	TCC	CAT	CCG	CAC
CIC	G	E	M	9	E	I	I
	GGG	GAG	ATG	66C	GAA	ATC	ATC
I ATC	P	N AAC	YTAC	A GCT	V GTG	F TTT	H CAC
L	E GAG	F TTC	K AAG	F	A GCT	S TCC	A GCT
P	R CGG	H CAC	S TCC	F	$_{ m L}$	R AGG	L
C	K	R	A	A	V	C	I
TGC	AAG	CGC	GCC	GCC	GTG	TGC	ATC
L CTG	L CIG	CIC	P	G GGA	D GAT	V GTG	V GTG
L	V	Y	K	N	E	T	R
CTG	GTG	TAC	AAG	AAT	GAA	ACC	CGC
FTC	E GAG	C IGC	$^{ m Y}$	K AAG	D GAC	V GTG	CIC
N	A	R	9	A	Y	T	L
AAC	GCT	CGC	990	GCC	TAT	ACC	CTG
A	$_{\mathtt{TAT}}^{\mathtt{Y}}$	9	R	L	I	V	Q
GCT		660	CGT	CIG	ATT	GTC	CAG
I	S	Y	N	L	T	G	E
ATC	AGC	TAT	AAC	CIG	ACC	GGG	GAG
9 66C	FITC	L	L	T ACA	CIC	L CTG	P CCT
I ATT	F TTC	S TCA	R CGC	$_{ m ITG}$	A GCC	L	C TGC
W TGG	A GCC	W TGG	S TCC	L	I ATT	T ACA	$_{ m F}$
L	Y	C	Q	P	$_{ m CTT}$	V	V
CTG	TAT	TGC	CAG	CCT		GTC	GTG
I ATC	L	R CGC	L	S TCA	V GTG	TACC	M ATG

Fig. 17.

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Fig. 17K

609 1946

Q CAG

I ATC

S TCT

TACG

 $_{
m T}$

L

A GCC

N AAT

E GAA

PCCT

LCTC

LCTG

GGT

G GGG

Q CAA

A GCC

L CTC

S AGC

A GCT

A GCT

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				1737301			
629	649 2066	669 2126	689 2186	709	729 2306	749	769 2426
SHCC	M ATG	Q CAG	Y TAT	R CGC	A GCC	P CCT	3 9 9
S TCA	T ACC	G GGA	L	H CAC	R CGG	A GCT	PCCT
9	S	E	A	W	A	G	D
9	AGC	GAA	GCC	TGG	GCC	GGA	GAT
A	H	W	H	V	9	P	T
GCT	CAC	TGG	CAT	GTA	9	CCT	ACA
V	A	V	L	H	E	R	I
GTA	GCT	GTG	CTG	CAT	GAG	CGG	ATC
V GTG	R CGG	S AGC	S AGC	R CGG	G GGA	P	G G G
N	R	S	M	E		A	GGT
AAT	AGG	AGC	ATG	GAG	GGG	GCA	
A	S	G	E	P	E	A	Y
GCA		GGG	GAG	CCT	GAA	GCA	TAC
I	9	S	T	E	D	C	R
ATC	9	TCC	ACA	GAA	GAT	TGT	CGC
L	Q	S	S	A	P	P	R
	CAG	AGC	TCC	GCT	CCT	CCC	AGG
SAGC	L	A	A	Q	A	Y	Q
	CIG	GCC	GCA	CAG	GCC	TAT	CAG
$^{ m L}$	D GAC	T ACA	Y TAT	A GCC	S AGC	S AGC	F
P	R AGA	R AGG	E GAA	Q CAG	E GAA	A GCT	GGC
E GAG	PCCC	A GCC	S TCA	Q CAG	G GGA	S TCT	5 5 5
S	L	D	L	K	S	R	H
	CTG	GAT	CTG	AAG	AGT	CGC	CAT
E	P	V	V	H	E	P	L
GAG	CCA	GTG	GTG	CAC	GAG	CCT	CTG
S TCT	P CCT	999	L CTG	L	D GAT	I ATC	A GCC
O	9	S	S	Q	S	S	T
CAA	66C	TCT	AGC	CAG	AGT	TCT	ACC
$_{ m L}$	R	355	Q	H	E	Q	T
	CGG	6	CAG	CAC	GAG	CAG	ACC
S	C TGC	T ACA	L CTG	M ATG	R CGG	P	E GAG

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Fig. 17I

789	2486	809 2546	817 2570	2649	2728	2807	2886	2962	3044	3123	3202	3281	3360	3439	3518	3597
Ω	GAT	L CIA		ACGG	3660	2222	4GTC	rgga	STIC	LTCT	CTAT	4GGA	CAGA	3666	CCL	STGT
田	GAA	E GAG		เรรร	CACT	SGAC	rgca2	3GCC.	GCAC	CTG	AACGO	rtt7	3GGA(SAAG(CAC	BACC
A	GCA	D GAT		3CCA1	CCAAC	CCCAC	CCCC	STTG(SACC	rgCT(CTC	CATC	ACAT(CCT	GTC	rAGGC
M	TGG	E GAG		SCCTO	GTG(ZATC	CTAC	3GAG(ACCTO	GCTJ	TCCC	TGCC	TGC	GTG	CTCI	\GGG1
ტ	CAT TIC TCT CGG CTG CCT CTT GGA GGG TGG GCA GAA GAT	P E P V P E E G S E D E CCT GAG CCC GAA GAG GGC TCG GAG GAT GAG		STCT	GGAC	GCCTAGGAACCGAGGGCACACGGGACTCTAGCCTCATCCCCAGGACCCCC	'ACA(CAAGCAGGGAGAACCTGTGCCAACTGTGGAGTTGGGGAGGTTGGGGCCTGGA	CCTCAATAGATGAGCAGGTCAGGCTGTGGCCCTTACCTCACCGCAGTTC	CTCCGCTTCTTGCACATCACTGGCCTGTGTGTGCTGCTTGCT	CAGC	SCCI	CACC	CGTCCCAGCAAAAGAGCTCTGGCCCGCATCTCGCTGTGCCCTGAAGGGGG	TACT	SAGCA
ტ	GGA	9 660		ומממנ	CCAAC	CTAC	CTTJ	GGAC	ופפכנ	FIGTO	SCGT	GCT	CCAI	ATC	SCICC	AGCG
H	CTT	E GAG		3CCA1	TGG	3GAC1	3CCA(ACTG1	3CTG1	SCCT	CTAC	\CTT	ACCC	CCGC	BACT	rcgg2
Д	CCI	E GAA		CCT	3TGC(CACGO	ract(3CCA2	rcag(ACTG(4GAC(AAAT?	CGT?	TGG	TGG	SAAC.
ıП	CIG	P CCC		3CTG(STCT	3GCA(CCAG	CTGT	CAGG	SATC	STGA!	ATGG1	CTTA	4GCT(CATG	3000
ሊ	990	V GTG		SACC	STGT(GAG	4GCC(SAAC	rgag(rgca(ragg(ZAGG1	3CTG(AAAG	ACTG(GCT(
ഗ	ICI	P) 1 1 1 1 1	STTT(SAACO	3CCC/	3GGA(raga:	LTCT.	3CGT	3GAG(CATT	4GCA4	TGC	ATTG(
Ĺц	\mathtt{TTC}	E GAG		\TGG	rggT(TAG	CCA	4GCA(CAA	CGC	TTT(rGTA(CCT	וכככז	3CTG(FIGA
H	CAT	PCCT	* TAG	CAGGA	rgrg1	36600	GICC	SCCA	CCCCI	CICIO	rttg(AAATT	1666	racg1	rrgg	AGTG(
ഗ	\mathtt{ICT}		V GTA	3600	CACG	LTTG	AACT(AGCT(ragco	ACCT	3GCT.	LTCT?	LTCC.	rgrg.	3GCT.	3GAG1
Д	CCC	R AGG	K AAG	CTGT() ೨೨ ೨ ೯	3GAA.	raga <i>i</i>	raga <i>i</i>	וכככו	SCTC	3TTC	AGGT.	3GTC.	rggc.	CGA	rttg(
>	GTT	S TCA	H CAC	STTC	CCTG	3AGA(3TGC.	ACGA.	ACCT.	3000	r _T CC(AAGA.	CTGA(ACCT.	rcgc	CGGC.
~	AGG	A GCA	V GTG	CAGG(STTC(CCAG	rgrg(3005	r GCA	rgca(CCG	AAAAI	3AGA(3GTG	rgccr	3GTC(
Д	ACA GIG CCC AGG GIT CCC TCT	G Q S A S R H GGG CAG TCG GCA TCA AGG CAC	P P Q V H K V CCC CCT CAG GTG CAC AAG GTA T	ACAAGGCTGAGCAGGGTTCCTGTGGCCCAGGATGGAGGCCACCGCTGCCCTGCCATCCCGTCTGCCTGC	CTCCTCTGAGTGTTCCCTGGCCCCACGTGTGTGTGTTTGTGTGTCTGTGCCTGGCCAAGGGAGGTGCCAACACTGGGC	TTGCCACAGCCCCAGGAGGAATTTGGG	TTGGCTCAGAGTGTGGTGCTAGAAACTGGTCCCCAGCCCCAGCCCCAGTACTGCCACCTTTACACCTACCCCTGCAAGTC	CCCAGAGGGCTGCCCACGATAGAAGCTGC	CCCTCAACCCCTGCAACCTTCCCTAGCCC	TCGCCCAGTGCTGCAGCCGGCTCACCTCT	GTTCGCTTGCTCCCGTTCCGTTTCGGCTTTTGCTTTGCGTTAGGGTGAAGACCCTAGCGTCCAGCTCCCCTCAACGCTAT	ATTITGACACTAAAAAGAAGGTITCTAAATTGTAGGAGCAGGATGGAAATACTTTGCTGCCCTTGCCATCTTTAGGA	TGGGCCCCCCAGGAGACTGAGGTCTTCCTGGGCCCTCATTGCTGCTTATCGTACCCCCCCATCACCTGCACATGGGACAGA	CCGGGCTGGAGGGTGACCTTGGCTGTGTA	ATGAAGGGCGATGCCTCGCCCGAGGCTTTGGGCTGCTGCACTGCTGGGACTGCTCCTACTCTCTGTCCCACCCCT	CACCCAGCTGTGGTCCGGCTTTGGGAGAGTGGTGAATTGCGCTGCCCGAACTCGGAGCGGAGCAGGGTAGGGACCGTGT
>	GTG	Q CAG	P CCT	AGGC.	CICI(CCAC	3CIC	4GAG(TCAA(CCCA	CGCT	TTGA(3000	3GCT(AAGG	CCAG
E-	ACA	G GGG	P CCC	ACAİ	CIC	${ m TTG}($	TTG(222	CCC	TCG	GTT(ATT	TGG(CCG	ATG.	CAC

Fig. 17M

CACCCAGCTGTGGTCCGGCTTTGGGAGAGTGGTGAATTGCGCTGCCCGAACTCGGAGCGGAGCAGGGTAGGGACCGTGT

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J. P. FINAL FROM

79 158 AGCGGCGTGGGGAAGACCTAGGGGGGGGGGGGGGGGAAGCAGACAGGAGAACACTCGAAATCAAGCGCTTTACAGATTA

229 ω TTA Ы ACT Н TIG \gt TCA ഗ ATG Σ AAC Z ATG Σ TTTTATTTTGTATAGAGAACACGTAGCGACTCCGAAGATCAGCCCCA

28 289 GAA 口 CAG Ø ATG Σ TGG ⋈ CAA O ATC Н GCC Ø GAA 闰 AAT Z GAG 冝 AAC Z TIC ഥ CAG Ø AAG \bowtie GAA 闰 TIC ഥ GAA 囜 TAT GAA 闰 CAA O

48 349 CGG ഷ GGT Ö GGT Ö TIC ഥ ATA \vdash TTT Ŀ GCC ø GCT Ø TAT \bowtie CIG Ц GCT Ø TCT ß TTT ᅜ CTG Ц TTC щ TCT വ AAA × AAG ¥ TGG ⋈ AAC

409 CTG TCT TGG CIC GIG TTA CCA AAG AGG CTG GAA TTT AAG GCA CGA AAA AAT ATG CTA CAC

88 469 ATT Н TAC × GIG > ATG Σ TAT \succ GCT ø GGT Ö ACT Η CGA α CTT Ы GCT Ø GGT Ç TIC ഥ ATA AGT വ TIC ſτι GIC \gt GCA Ø LCTT ACC Η

108 529 GTC > CCL Д GGA Ö AAT Z TAC \succ TTT ഥ GGT Ö CAG Ø GAC Д TGI C GTT > TCA വ CAG Ø AAG 노 CIG П 969 Ç AAA 노 ACC Н ATG Σ TIG Ц

128 589 ATA Н ACA Н GAT Ω GGA Ċ CTA Н GAA 团 CCC വ GCA ø AAA ¥ AGC ഗ CTA Ц GIG > TTT ഥ GCA ø TAT × GCT Ø TGG ⋈ TIC ഥ AAA ¥ AGC വ

18A

148	4	168	709	188	9	208	829	228	889	4	949	266	1003
> 5	5.T.5	⊱	ACT	Ĺτι	TTC	Σ	ATG	Ħ	CAC	H	CAT		•
E C	ACI.	Σ	ATG	ප	GGT	П	CTG	ഗ	TCT		IGC		
H É	AIC	ഥ	TTC	Ø	GCA	Σ	ATG	H	CAC	দ	TTC	*	TAG
ΞĘ	CAC	Z	TGG	Ø	GCG	Q	CAG	บ	TGT	П	CIC	ы	GAA
. T	CAC	ტ	GGT	ద	CGG	Н	ACT	Ø	CAG	>	GTG	Ø	GCT
>	TAT	ტ	GGA	ц	TTG	н	ATC	Ω	GAC	П	CLL	X	AAA
7 ≥ ₹	5.5.T	ტ	GGG	Ø	GCC	Ø	CAG	н	CAT	×	TAC	⊱	ACG
Ήć	CAC	Ø	GCC	≯	TAT	ഗ	ICC	Ø	CAG	Ø	AGC	₽	ACA
υĘ	5 T.	>	GTT	≯	TAC	П	TTG	Σ	ATG	J	CIC	ೱ	AAA
ъ E		Σ	ATG	Ø	TCT	Н	ACC	Z	TGG	×	TAC	ద	AGG
H E	AIC	Ω	GAC	⊱₁	TAC	н	ATC	บ	IGC	Σ	ATG	Σ	ATG
i E	S.T.O.	×	AAA	Σ	ATG	ഥ	TTC	ഥ	TTC	Ы	CIC	노	AAA
X 4	AAG	×	TAC	>	GTG	Σ	ATG	>	GIC	വ	TCA	ტ	GGC
ر م ج	CAG	ഗ	ICC	Ø	CCC	Ø	ದಿದ್ದ	긔	CIG	ഗ	ICC	н	ATC
以 以 (AAG	×	TAC	н	CAC	ഥ	TTT	×	TAC	Z	TGG	×	TAC
자 (AGG	Z	TGG	>	GTG	×	AAG	Z	AAC	ᅜ	TTC	Ø	GCC
цĘ	Ď. Σ	വ	TCT	IJ	GGC	ద	CGG	>	GTT	Н	ATC	臼	GAG
ΗĘ	ATT	×	TAC	×	TAT	യ	ICC	>	GTG	Z	AAC	Ĺτι	TTT
ΗĘ	ATT	ц	CTG	Z	AAC	>	GIC	ט	TGT	Ø	CAG	Щ	TTC
بر <u>ا</u> د	D.I.I.	П	CIC	Σ	ATG	ద	CGA	ტ	GGC	ſΞţ	TTT	ഥ	TTC

TGTTGGAACTGAGGAGGAAGCCATAGCTCAGGGTCATCAAGAAAATAATAGACAAAAGAAAATGGCACAAGGAATCAC 1082 ACGTGGTGCAGCTAAAACAAAACAAAACATGAGCAAACACACAAAACCCAAGGCAGCTTAGGGATAATTAGGTTGATTTAA 1161

2188 2346 2425 2820 2978 1398 1556 1635 2030 2109 2899 1477 1714 1793 1872 1951 2267 2504 2583 2662 2741 CCCAGTAAGTTTATGATCCTTTTAGGGTGAGGACTCACTGAGTGCACCTCCATCTCCAAGCACTGCTGCTGGAAGACCC IGTCAATGTTTCTAGTATTTCAAAGAAGCAATTATGTAAAGTTGTTCAATGTGACATAATAGTATTATAATTGGTTAAG IAGCTTAATGATTAGGCAAACTAGATGAAAAGATTAGGGGGCTTCCACACTGCATAGATTACACGCACATAGCCACGCAT AAAAAACAAAACCAAAACTGTTGTTTCTCTCTTTGCTTTTGAGAGTGTACAGTAAAAAGGGATTTTTTCGAATTATTTTA TATTATTTTAGCTTTTAATTGTGCTGTCGTTCATGAAACAGAGCTGCTCTGCTTTTCTGTCAGAGATGGCAAGGGCTTTT ACAAAGGCTATTAACACATAGGAAAAATGTATTTACTAAGTGTCACATTTCTCTAAGATGAAAAGATTTTTACTCTAGA <u>AGAGACACAGGGTGTATATCTAGAACGATAATGCTTTTTGCAGAAACTAAAGCCTTTTTAAGAAATGCCAGCTGCTGTA</u> SACCCCATGAGAAAAGATGTCTTAATCATCCTTATGAAAACAGATGTAAAACAACTATATTTCAACTAAACTTCATCTTCA CTGCATAGCCTCAGGCTAGTGAGTTTGCCAAAACCAAAGGGGGGTGAATACTTCCCCCAAGATTCTTCCTGGGAGGATGGA AACAGTGCAGCCCAGGTCCCATGGGGGCAGCTCCCATCCCAGAGCATTTCTGATAGTTGAACTGTAATTTCTACTCTAA GTGAGATATGAAGCATTATCCTTTTGTTCAGTTGCCCCGGGCTTTTGAACAGAAGAGTAAATACAGAATTGAAAAAAGAT AAACACTCAACCAAACAATGTGAAAACGGGTTCTGTAGTATTTGTAAAAAGGCCCGGCCCAGGACCACTGTGAGCTGGA TGACTICACACACTCATAACTTICCAAAIGAAACCCCACAGIAIAAGCGCAIATITICGAIAITITIGIGAAITICCAA AAGGAAATCACAGGGCTGTTCGAAATATTGGGGGAACACTGTGTTTCTGCATCATCTGCATTTGCTCCCCAAGCAATGT SACAACAAAGGGCCCCCATACACTTATCCCTCAAATTTTAAGTGATATGAAATACTTGTCATGTCTTTGGCCAAATCAG TAAGAGCCATATTCTTTAAAAAAAAAAAAAAATATTCTCTCTGTAATATTTTCAGTCCTTTACAAGCCAAATACATG ACACACACAGACACACAGATGTGGGGGTACACTGGAACTTCAAAGCCCAAATGAATAGAAACACATTTTCTGGCTAGCAGA **AGAGGTGTTTTAAAGGGCCCTCTGCTGGCTGAGTGGCAATACTACAACAAACTTCAAGGCAAGTTTGGCTGAAAACAGTT** AAGATATTCATCCTGCTTCAAGTCAGCTTCAGAAATGTTTTAAAAGGGACTTTAGCTCTGGAACTCAAAATCAATTTAT AAAAAAAAAA

19	39	59 179	79	99 299	119 359	139 419	159 479
W	CTG	S TCC	ე ენე	R CGG	I ATT	Q CAG	${\mathtt F}$
F	I	Y	Y	S	V	F	F
TTC :	ATT	TAC	TAT	TCC	GTC	TTT	TTC
K	I	L	N	V	C	H	H
AAA 1	ATC	CTG	AAC	GTC	TGT		CAT
S	F	CIC	M	R	g	S	C
AGC A	TTC		ATG	CGA	GGC	TCC	TGC
V	I	V	TACT	F	M	Y	F
GTC A	ATA	GTG		TTC	ATG	TAC	TTC
P CCT (T ACG	T ACT	M ATG	G GGT	L	C TGC	CIC
GGA (D	I	F	A	M	Q	V
	GAC	ATC	TTC	GCG	ATG	CAG	GTG
N	G	H	W	A	Q	D	L
AAT (GGT	CAC	TGG	GCT	CAG	GAC	
Y TAC A	L CTA	H	GGT	R CGG	TACT	N AAC	Y TAC
F	E	Y	G	L	I	D	S
TTT :	GAA	TAC	GGT	TTG	ATC	GAC	AGC
S AGT	P	W TGG	ტ ტტტ	A GCC	Q CAG	H CAT	L
Q CAG 1	A GCA	H	A GCT	Y TAC	S	Q CAG	Y TAC
D	K	L	V	Y	L	M	M
GAC (AAA	CTG	GTC	TAC	TTG	ATG	ATG
C TGT (S AGC	F TTC	M ATG	S	T ACC	W TGG	L
V	L	I	D	Y	I	N	S
GTT		ATC	GAC	TAC	ATC	AAC	TCG
S	V	L	K	M	F	F	S
TCA (GTG	CTG	AAA	ATG	TTC	TTC	TCC
Q	F	K	Y	V	M	V	W
CAG	TTT	AAA	TAC	GTC	ATG	GTC	TGG
K AAG (A GCA	Q CAG	S	A GCC	A GCC	L	${ t F}$
L	Y	K	Y	H	F	Y	I
CTG A	TAT	AAA	TAC		TTT	TAC	ATC
0 00	A	R	W	V	K	N	N
	GCT	AGG	TGG	GTG	AAG	AAC	AAC

Fig. 18E

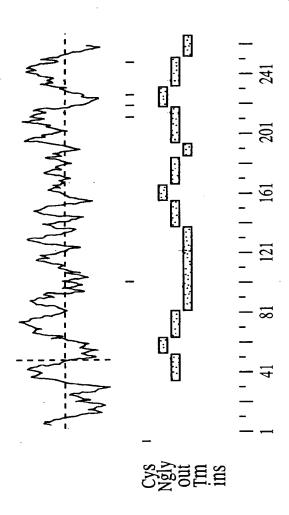


FIG. 18D

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1475 1554 1633

CCATCGTCCCTGGAGCTGAACAGGGAAGGGCTATGGGCAGAGACTAGAGCCGGATTCATCCAATGTGCAGACAGCG <u>IGTTCGCCTCCCTCCTGTTCGACCTCACATAATCCTGGCTTTCTAAATGAGGCCCTGTGACACACTCTGTGCTTTC</u> PATATITITIGIGACITICAAACACAGATCIGCAGGGCICIGCCIGATITIGGGGGTAAACACIGIGITITCIGCAGCCICIG CATITIGCTCCCTTCAGCAGTGCAGAGGCTTGAGAAGTGCCCTCTGCTGGCTTAGTGAGAAGCTTCAACAAAACACTTCAC AGTAGGTTGAAATAACTGACCACTAAGGGCCCTGCGGAGATTAAACCCTAAGTTCTAAGTGCTGTCAAACACCTGACATA PATITIGACCAAATCAGAAGAGAGAGAGACCTCTATGCTTCAAGTAAGCGTCATAAATTTTTAAGTGACTTTCACTTG

1712

1791 1870 1949 2028

2032

1080 1159 1238 175 909 685 764 843 922 1317 1396 527 1001 TGACAACTGTTATTTCTGCTCTCCGACGAGAATTCAAGCATCCGTTGTTCAGTTGCCCCCAAACTTTAGGACGGAGGAGT AATTATTTTACTGCAACTGAAAGTAAAGAGGTAGAGCCTTTCCCCCTTCTGCACAGGCCTTGTATGTTCTCTT CATATGGTGCAGCTAAAACAAAACAAAACATCCGTATGAGCAGGCACGAGGCCCAAGGCAGCTTGGGACTGAAGATTAG STIGIAAGITITAIGAICCIITICIGGGIGAGGACICGCIGAGIGCAACICITAICICAAAGCACGGCIGCIGAGGGAC CCTTCCCTCTGGCCTGTCAACTCTAGAACACACTAGATGCAAAGGCAGCCACGGGCAAAGAGAGATTGGGCAGAGAGATTAGT GGACGGCCAGCAAAACACTGCAGGAAGCAGGTGGGGGGGAGGAATCTACTCAGCCTTTTTTGTTTTGTTTTGTTTTGTTTT CACACACACACGCCAATCTTTCAACACGAAACCAGAGCTAAAAGAAAAGATAAACATGGGAGAGACAGGGTTTCTAT Y I G K V K K A T K A E TAC ATC GGC AAA GTG AAG AAA GCC ACG AAG GCT GAG

Fig. 18]

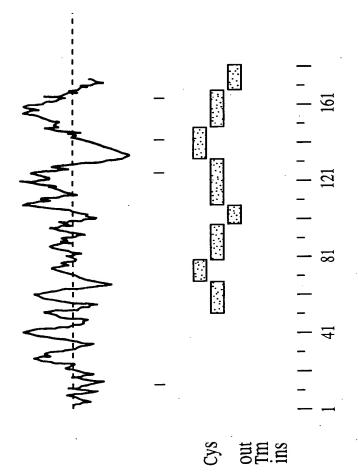


FIG. 186

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70 TL	1 () 년 · 년	0	ن	ņ				
20 30 40 50 60 70 FNENEAIQWMQENWKKSFLFSALYAAFIFGGRHLMNKRAKFELRKPLVLWSLTL		GLKQSVCDQGFYNGPVSKFWAYAFVLSKAPELGDTIFIILRKQKLIFL :::::::::::::::::::::::::::::::::::	210	KDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQITQMLMGC	::::::::::::::::::::::::::::::::::::::				
PLVL		LRKQ] :::: LRKQ]	2	ITOI	E:::	0			
60 LRKI	C	7	200	TLS	TLSC	110			
AKFE		GDTI :::: GDTI	N	AMFI	:::: AMFI		KAE	::: KAE	
MNKR	 	APEL :::: APEL 30		SRKF	SRKF	100 260	RKTT	···: KKAT	170
50 GRHL		VLSK ::::: VLSK	190	3FRV.	SFRV	0	IGKM	:::. IGKV	
FIFG(4YAF' :::: 4YAF'	,	.RAA(:::: JRAA(0	FEAY	FEAY	0
40 LYAAI	; ; ; ; ; ;	SKFWA ::::: SKFWA	180	SYYAI	SYYAI	90 250	HFF	HEF	160
, FSAI	-	IGPVS	18	VMYS	NWYS		VLFC	.::: VLFC	
KSFI		GFYN :::: SFYN 10) H	GVH.	:::: 'GVH <i>I</i>	0 0	LSYL	::::::::::::::::::::::::::::::::::::::	150
30 ENWK			170	TMNY	:::: IMNI	240	SLMY	SI.MY	Н
QWIMQ	 	LKQS :::: LKQS		GWFM	GWFM		IFWS	:::: IFWS	
O NEAI	 	MTKG 	0	VAGG	VAGG	70 230	HFQN	HFQN	140
20 2FNEN	Ι Ο Ι Ο Ι .	YILI	160	YKDM	:::: YKDM) CHS	:::	
FEK(3AYM		SWYS	SWYS	09)Q	:: HDND(130
10 QEYE	; ; ; ;	ILRIC	150	7LLYS	HWYHHITVLLYSWYS::::::::	220	WMQF		<u> </u>
VLTI		IFGA	П	HITV	:::: HITV	C	LVFC	LVFN	
10 human MNMSVLTLQEYEFEKQ	! ! !	human AVFSIFGALRTGAYMVYILMTKGLKQSVCDQGFYNGPVSKFWAYAFVLSKAPELGDTIFIILRKQKLIFL :::::::::::::::::::::::::::::::::::		human HWYHHITVLLYSWYSY)	######################################	20	human VVNYLVFCWMQHDQCHSHFQNIFWSSLMYLSYLVLFCHFFFEAYIGKMRKTTKAE		120
man	ine	human murine		man	ine		man	murine	
hul	murine	humur		hu	mur		hu	mur	

Fig. 18H

COPERTO CHERON

70 300	 	140 TGG	 	210 CTT	! !	280 GCC	ر ر
CCAT	1	1 CGGT	 	2 Accc	!	230 240 250 260 270 280 TTCGGTGCTCTTCGAACTGGTGTTATATGGTGTACATTTTGATGACCAAAGGCC	
) rgaag	1) ATATI) CTCTG) BACCP	
60 AGAAT	; ; !	130 CTTTA		200 rggtc		270 rgarg	; ;
AACG.	i i	CTGC	 	GCTC	 	ATTT	
50 GTTC	 	120 TATG	 	190 'TAGT	 	260 GTAC	1 1 1
AAGCA	1	TCTG	 	CCAT	 	TGGT	1
40 CGAAA		110 TTCTG(180 AGGAAG	t 1 1	250 CTTAT?	
, AATT(1. GTTT:	 	1{ CTGA(; ; ;	GTGC!	
TATG	 	TCCT	 	TGAA	 	ACTG	† †
30 AGAA	 	100 TCTT	1	170 AGTT	 	240 TCGA	
LTACA		1GAA?		1GCA.		GTCI	
20 3ACT1	! !	90 TGGAA		160 AACG2	 	230 'CGGTC	; ; ;
TGTT	1 1 1	AAAC	 	AATA	 	TATT	
10 GTCAG	1	80 CAGGA	 	o Paatg	 	o AGTA	
1 ACATG		8 BATGC	 	150 CACCTA	1 	220 rcttca	
10 20 30 40 50 60 70 human ATGAACATGTCAGTGTTTACAAGAATATGAATTCGAAAAGCAGTTCAACGAGAATGAAGCCATCC	 	80 90 100 110 120 140 human AATGGATGCAGGAAAACTGGAAGAAATCTTTCCTGTTTTCTGCTCTCTGTTTTATATTCGGTGG	; ; ; ;	150 160 170 180 190 200 210 human TCGGCACCTAATAAACGAGCAAAGTTTGAACTGAGGAAGCCATTAGTGCTCTGGTCTCTGACCCTT	; ! !	220 human GCAGTCTTCAGTATA'	 - - -
man i	murine .	man i	murine	man .	murine	man (murine
hu	mur	hu	mur	hu	mur	hu	mur

Fig. 18

350 CATTTGT :::::: CATTTGT 70	420 TTCCTG :::::: TTCCTG	490 GGGGGAG :::::::	560 3GCAGG ::.:: TGCGGG 280
340 FGGGCTTATGC:::::::	370 380 390 400 410 42 CGAACTAGGAGATACAATATTCATTATTCTGAGGAAGCAGAAGCTGATCTTCCT :::::::::::::::::::::::::::::::	440 450 460 470 480 490 ATCACTGTGCTCCTGTACTCCTACAAGACATGGTTGCCGGGGGAG :::::::::::::::::::::::::::::	510 520 530 540 550 560 IGAACTATGGCGTGCACGCCGTGATGTACTTACTATGCCTTGCGGGCGG
300 310 320 330 340 TGACCAGGGTTTTTACAATGGACCTGTCAGCAAATTCTGGGCTTAT ::::::::::::::::::::::::::::::::::	400 CTGAGGAAGC2 ::::::::::::::::::::::::::::::::::::	460 470 48C TGGTACTCCTACAAAGACATGGTT :::::::::::::::::::::::::::::::::	540 CTCTTACTATC :::::::: CTCTTACTACC
320 \ATGGACCTGT \::::::::: \ATGGACCTGT	390 :ATTCATTATT :::::::::::::::::::::::::::	460 CTCTTGGTACT ::::::::	510 520 530 540 TGAACTATGGCGTGCACGCCGTGATGTACTTACTA::::::::::
310 3GGTTTTTAC? 3AGTTTTTAC? 30	380 3GAGATACAA1 ::::::::: 3GTGACACGA1	440 450 ATCACTGTGCTCCTGTACTCT :::::::::::::: ATCACTGTGCTCCTGTACTCT 160 170	520 rggcgrgcACC ::::::::::
300 FTTGTGACCAC::::::::::::::::::::::::::::::	370 ACCCGAACTAC ::::::::	440 CACATCACTG1 ::::::::: CACATCACTG1	510 CTATGAACTA: :::::::::::::::::::::::::::::::::
290 310 320 330 340 350 350 340 350 350 340 350 human TGAAGCAGTTTTGTGACTTTTTTTTTTTTTTTTTTTTTT	360 370 380 400 400 420 human GCTAAGCACCCGAACTAGGAGATACAATATTCATTATTCTGAGGAAGCAGAAGCTGATCTTCCTG :::::::::::::::::::::::::::::::	430 440 450 460 470 480 490 490 human CACTGGTATCACTCTGTACTCTTGGTACTCCTACAAAGACATGGTTGCCGGGGGAG :::::::::::::::::::::::::::::	500 human GTTGGTTCATGACTA :::::::::::::::::::::::::::::::::::
human murine	human murine	human murine	human murine

Fig. 18.

human murine	570 580 600 610 620 630 human TTTCCGAGTCTCCCGGAAGTTTGCCATGTTCATCATCTTGTCCCAGATCACTCAGATGCTGATGGCTGT ::::::::::::::::::::::::::::::::	580 CCGGAAGTTTG	590 CCATGTTCA1 ::::::::::::::::::::::::::::::::::::	600 CCACCTTGT(:::::::: CCACCTTGT(610 CCCAGATCAC ::::::::: CCCAGATCAC	580 620 600 610 620 630 AAGTTTGCCATGTTCACCTTGTCCCAGATCACTCAGATGCTGATGGGCTGT ::::::::::::::::::::::::::::::	630 TGGGCTGT ::::::: TGGGCTGT 350
human murine	640 650 670 670 690 human GTGGTTAACTACCTGGTCTTCTGCTGGATGCAGTGACCAGTGTCACTCTCACTTTCAGAACA ::::::::::::::::::::::::::::::::	650 CTGGTCTTCTG ::::::::::	650 CTTCTGCTGGATGCAGCATGAC ::::::::::::::::::::::::::::::::::::	GCATGAC :::::: GCATGACAA(390	670 CAGTGTC :::: CGACCAGTGCT 400	670 680 690CAGTGTCACTCTCAGAACA ::::: :::::::::::::::::::::::::::::	690 TCAGAACA ::::::: TCAGAACA 420
human murine	700 710 720 730 740 750 760 TCTTCTGGTCCTCACTCTCAGCTACCTTGTGCTCTTCTGCCATTTCTTTTGAGGCCTACAT ::::::::::::::::::::::::::::::::	710 CACTCATGTAC :::::::::::	720 CTCAGCTACC ::::::::::::::::::::::::::::::::::	730 CTTGTGCTC ::::::::: CTTGTGCTC 460	740 FTCTGCCATT :::::::: FTCTGCCATT	720 730 740 750 760 CATGTACCTCAGCTACCTTGTGCTCTTCTGCCATTTCTTTTTGAGGCCTACAT ::::::::::::::::::::::::::::::::	760 GCCTACAT ::::::: GCCTACAT 490
human murine	770 780 790 human CGGCAAATGAGGAAAACAACGAAAGCTGAA :::::::::::::::::::::::::::::::::::	780 GGAAACAACGA :::::::::: AGAAAGCCACGA	790 ACAACGAAAGCTGAA .: :::::::::: GCCACGAAGGCTGAG 520				

Fig. 18K

0 0.		O O	
LQRP : : LRKP 60	AFIII :::: FFIII 130	TELÇ :: : : TLSÇ 200	O . 19
SFSI : :	OTAI	(VI)	270 SKSÇ .: IKAE
60 FRKS : KRAK	130 31.GE ::::	200 LLPN : KFAN	270 PKGKVASKSÇ : : SKMRKTTKAE 260
FYMR7 : HLMNF 50	(VVI) : (API)	HPNI · /SRI	PKGI : SKMI
3QT) : . 5RHI 5	.:::. /LSKA	KLKHE 3FRVS	260 AYLRI ::. AYI-C
50 IVVC : .	120 SFLFI :	190 MKAA! :: LRAAC	2 HRAN
LLLL	1 FWS] ::.	YTMI	HFFH ::: HFFF 250
VVYL : ALYA 40	VVRF : .: VSKF 110	YTYY :-:: YSYY 180	50 LFAI :: LFCI
40 FLIV ::.	110 120 130 YTDDAVVRFWSFLFLLSKVVELGDTAFII: .::. :::: ::: ::: FYNGPVSKFWAYAFVLSKAPELGDTIFII 110 120 130	180 VHSVM::.:: VHAVM	250 YFILF :: YLVLF
XSS F:: FST	11 IYT. GFY	16 GVH :::: GVH	LYGT .: . MYLS 240
20 30 40 50 60 MQPYDFET-FQDLRPFLEEYWVSSFLIVVVYLLLIVVGQTYMRTRKSFSLQRP ::::::::::::::::::::::::::::::::::::	70 80 100 100 110 120 130 LILWSFFLAIFSILGTLRMWKFMATVMFTVGLKQTVCFAIYTDDAVVRFWSFLFLLSKVVELGDTAFIIL :.::.::.::.::.::.:::::::::::::::::::	140 150 160 170 180 190 200 RKRPLIFVHWYHHSTVLLFTSFGYKNKVPSGGWFMTMNFGVHSVMYTYYTMKAAKLKHPNLLPMVITSLQ ::.::::::::::::::::::::::::::::::::::	210 220 230 240 250 260 270 ILQMVLGTIFGILNYIWRQEKGCHTTTEHFFWSFMLYGTYFILFAHFFHRAYLRPKGKVASKSQ : ::: . : : : : : : : : : : : : : : :
TEE THOE	ASÕ3 . · : CÕLA	0 IFMT :::: IFMT	240 FWSF:::
30 PF AIQW	100 /GLKÇ ::::	170 3GGWF ::::	rtehe HPQN1 230
FQDLRE: FNENEZ	90 100 FMATVMFTVGLKQTVCE .: :::::: YMVYILMTKGLKQSVCI 90 10	NKVPS : OMVAC 160	HTTJ::. HSHI
-FOI :-	ATVP VYII	YKNI ::. YKDN	230 KGCHT: ::· DQCHSI
20 QPYDFET- : :.:: QEYEFEKÇ 10	90 KFM <i>Z</i> .:.	160 SFGY : WYSY	RQE] : MQH]
20 2PYDF : : .: 2EYEF	LRMW: :: LRTG: 80	LFT: : LYS:	:0 LNYIWRQE : : : LVFCWMQE
	GTLRN :-:: GALRT 80	TVLLE ::::: TVLLY 150	220 31LN . : NYLV
KMD TL-	80 SIL ::.	150 YHHS ::: YHHI	210 LQMVLGTIFG ::: TQMLMGCVVN
10 RGL : :	AIF: : : : .:	O XMH' ::: XMHL	TLGTI .: . MGCV
INFS	FELP: . :: SLTLP	. FVE: . : . : . I FLE: 140	210 ILQMV : ::. ITQMI
TSIV ::	70 80 LILWSFFLAIFSIL :.::::::::: LVLWSLTLAVFSIF	140 2KRPLIFVHWYHH: 1. 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:	2 11 (
M	Z : Z	1 0 RF	210 220 230 240 250 260 270 I400 ILQMVLGTIFGILNYIWRQEKGCHTTTEHFFWSFMLYGTYFILFAHFFHRAYLRPKGKVASKSQ : ::: . : : : : : : : : : : : : : :
10 I400 MDTSMNFSRGLKMDL :.:.: CIG30 MNMSVLTL	1400 CIG30	140 150 160 170 180 200 I400 RKRPLIFVHWYHHSTVLLFTSFGYKNKVPSGGWFMTMNFGVHSVMYTYYTMKAAKLKHPNLLPMVITSLQ ::.::::::::::::::::::::::::::::::::::	· · · · · · · · · · · · · · · · · · ·
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Fig. 18L

in in a factor of the factor o

	C	1001 10	80 -ATGCAGGAAAACTGGAAGAAATCTTTCCT-GTTTTCTGC-TCTGTATGCT	CTTTTTGGAGGAGTACTGGGTAAGCTCATTTCTCATAGTGGTCGTCTATCTGTTT	140 190	GCCTTTATATTCGGTGGTCGGCACCTA-ATGAATAAACGAGCAAAGTTTGAACT-GAGGAAGCCATTAGT	CAT	200 210 220 230 240 250 260 GCTCTGGTGTCTTATATATGGTGTGTGTGTGTGTGTGTATATACTTATACTTACT	
	GAAG	44GF	120 GTAT	CGTCTATCTG	П	CATI	CTCI	2 3GTQ ::: .	0
9	AAT() -	TCT	::: TCT		AGC(.GGCC'	O TATATGG :.::::	270
	CGAG	60 60	rgc-	3TCG	180	AGGA	CAGA	250 CTTA :.	
	CAA(CIA.	110 TTC:	GTG	, ,	T-G2	TTG(0	GTG(: . GGA	0
50	AGTT) (-GTT	·:· :ATA		BAAC :.:	AGCT 190	ACTG	260
	CGAAAAGCAGTTCAACGAGAATGAAGC	19CA	CCI.	.:::::::::::::::::::::::::::::::::::::	170	TTCGGTGGTCGGCACCTA-ATGAATAAACGAGCAAAGTTTGAACT-GAGGAAGCCAT	CTTC	210 230 240 250 260 CTTGCAGTCTTCGAACTGGTGCTTATATGGTGTGTAC :::::::::::::::::::::::::::::::::::	
	AAA 	45 T.	100 CTTT	.:: 'ATT'	러	AAG'	GAG	CTT	0
40) t)	1 AATC	. :: GCTO	o	AGC?	3A-AG, 180	1GC1 : - : : IAC1	250
	- III	40 40	AGA	:. TAAG	160	ACG.	GCG	230 'CGG' ::	
	TGAA		90 IGGA	:::. IGGG	н	ATAA 	3AAC 0	ratt : : rcci	240
30	TTACAAGAATATGAATT	30 30	AAC	TAC	>	TGA	TGAG	220 TTCAGTATZ :::::::	Ö
m	AAGA	9 9 5 5	3GA.P	::::: 3GAGT	150	ra-a	raca	220 LTCA(::::	
	TAC.) 1	80 GCA(: : GGA(; ;	ACC	ACC.	GTC.	230
20	ACTT	11C1	AT	·: TTTT	D	7.GGC	2AG-A 160	210 CTTGCAGTC :: :::.: CTGGCAATA	7
	TTGZ		! !	CCTJ	140	GGTC	255	210 CCTT ::: CCTG	
	AGTG	Ď TY.	- 99 -	. : : \GGC	Н	GGT.	GTT)	GAC 	220
10	GTCAGTGT	A10	70 CCAAT	.: .:.:: ACTTAAGG) 0	ATT(CGTT	0 CTCI : :	
	CAT) (A)	7 TC	· :	130	TTATA	CAT	200 CTCTGGTCT :::::::	
	ATGAACA'	1 555	70 CATCCAATGG-	:: .:.:: TTCAGGACTTAAGGCC	П	CCTJ	C1	200 GCTCTGGTCTCTGACC :::::::::::	210
	I400 ATGAACATGTCAGTGTTGACTTTACAAGAATATGAATTCGAAAAGCAGTTCAACGAGAATGAAGC- ::::::::::::::::::::::::::::::::::::	⊄				G	CIG30 GCTCATCGTTGTTGGCCAG-ACCTACATGAGAACGCGGA-AGAGCTTCAGCTTGCAGAGGCCTCTCAT 150 150 160 170 180 190 200		
	I400 ATGAACATGTCAGTGTTGACTTTACAAGAATATGAATTCGAAAAGCAGTTCAACGAGAATGAAGC :::::::::::::::::::::::::::::::::::	, 5 7	1400	CIG30		I400	CIG	I400 CIG30	

Fig. 18M

270 280 300 310 320 I400 ATTTTGATGACCAGGCCTGAAGCAGTCAGTTTGTGACCAGGGTTTTTTACAATGGAC-CTGTCAGCA .: .:.:::::::::::::::::::::::::::::::	330 340 350 360 370 380 390 I400 AATTCTGGGCTTATGCATTTGTGCTAAGCACCCGAACTAGGAGATACAATATTCTGAG .::::::::::::::::::::::::::::::::::	400 410 420 430 440 450 460 I400 GAAGCAGAAGCTGATCTTCCTGCTACTGGTATTCACCATCATGTGCTCCTTGTACTCTTTGGTACTCCTAC :::: ::::::::::::::::::::::::::::::::	470 480 530 I400 AAAGACATGGTTGCCGG-GGGAGGTTGGTTCATGAACTATGGCGTGCACGCCGTGATGTACTCT :::::::::::::::::::::::::::::::::
320 AC-CTC ::::	370 380 390 GAACTAGGAGATACAATATTCATTATTCTGA ::::::::::::::::::::::::::::::::::::	460 TGGTAC .: :. AGCTTJ	530 GTGATC :::::
310 320 TTTACAATGGAC-CT:::::::::::::::::::::::::::::::::::	ATATT . :: GCCTT 400) !ACGCC(!ATTCT(540
310 FTTTAC :. :: CTACAC	380 3ATACA :::::	450 rccrgi : :::: racrgi	520 3CGTGC :::::
AGGGTT : : ATC 320	TAGGA(:.::: TGGGA(390	TGTGC7 .::::: AGTGC7 460	0 CTATGG ::.:: CTTTGG
300 TGACCA : .:::	370 CGAAC :::: TGAAC	440 ATCACI : :::	510 'ATGAAC' :::::: 'ATGAAC'
: :: ::: ::GTGCT 310	AGCACCO	430 440 450 460 CACTGGTATCACCACATCACTGTGCTCCTGTACTCTTGGTA :::::::::::::::::::::::::::::::::	500 CATGACTA' ::::::: 'CATGACCA'
290 AAGCAGTCAGTTTG :::::::::: AAGCAAACCGTGTG	360 AGCAAA(:::::. AGCAAG(0	430 GGTATC ::::: GGTACC	5 TGGTTC ::::: TGGTTC 510
BAAGCA ::::: CAAGCA 300	350 360 ITTGTGCTAAGCAAAG :::::::::::::::::::::::::::::::	420 CTGCACTG : :::: GTCCACTG	490 GGGAGGTT :::::::
280 GGCCTG :::::	35 GCATTTC ::: CTCTTTC	47 CTTCC: ::: CTTTG:	.: .: .: .: .: .: .: .: .: .: .: .: .: .
270 ATTTTGATGACCAAAG : .:.:::::::::::::::::::::::::::::::::	340 CTTATG : :.: CCTTTC 3	410 .GCTGATC .:::::	480 GTTGCC :::::
270 IGATG? ::.: : IGTTI?	340 AATTCTGGGCTTAT .::::::::::::::::::::::::::::::::::	CAGAAC :. :GTCCA	480 AAAGACATGGTTGCC ::::.::: AAGAACAAAGT-GCC 490
ATTT' .:. GTGA' 280	330 AATT(.::: GATT(400 GAAGCA ::::. TAAGCG	470 AAAG; :: AAGA;
1400 CIG30	1400 CIG30	1400 CIG30	1400 CIG30

Fig. 18N

CC :: CCTG	670 ACCAG :	740 TTCTG :::	
600 TTGT(6. TGA(CTCT.::::CTAT.	
ACCI ::::	AGCA::::AGGA(STGC	
ATCA(:::: ATCA(610	660 ATGC; : :: AGGC;	730 CTTGTG : .: TTCATC	.: :: :- AA
590 GTTC : ::	6 TGGA :::: TGGA	CAGCTAC : ::: SACCTAT	790 AAGCT .::: .GAGCC
590 CCATGITCATCACCT ::::::::: CCCCATGGTCATCACCA 600 610	CTGCT(:. :: CATCT(670	720 CTCAG : GGGAC	7 -GAA .:.
.: :: ::	650 CTT(:.	77 'ACC': 'ATGO	: - : : - : 'ATC(
580 AGTTT . :: .TCTTC	CTGGT::	ATGTA: :-:: CTATA: 730	780 AAAAC; : GTTGC; 800
5 GGAA .:. TAAT 590) FACÇ : ATAC 6	710 ACTC . : TATG	770 780 790 790 790 790 790 790 790 790 790 79
:: ::	640 'AACT' :. 'GGCA'	CTC2	ATG2
570 GTCT	GGTT :: CTTT	GGTCC' :::: GGTCT' 720	770 CAAAA' :::: CAAGG
570 580 CCGAGTCTCCCGGAAGTTTG : :: .: .: .: :: CTGAAGCATCCTAATCTTCT 580 590	0 630 640 650 660 67 TGATGGGCTGTGGTTAACTACCTGGTCTTCTGCTGGATGCAGCATGA : ::::: :::::::::::::::::::::::::::::	700 710 TCTTCTGGTCCTCACTCA ::::::::::::::::::::::::::::::::::::	1 DD 50
) TTTT: .AA(6. 16CTC 15. 16CAC	TC :: .CTTC	760 GCCTACATCGG ::::::::: GCCTACCTCAG
560 CGGCAGGT' : :: CTGCCAAA	ATGG ::: CTGG	90 AGAACA- :::::	0 TACA ::: TACC
GCGG :: : GCTG 570	620 GCTG : :	690 CAGA : . : : CGGA	760 3GCCT;
. : 3AAG() GATC ::: GATC	.CTTTC : :CAA-(TGA(770
550 CTTGC :: TATGA	T-CAG : ::: TGCAG 630	TCAC . :: A-AC	750 TTCTT ::: .
4TGC : .: 4CAC	610 TCAC : .: T-TC	680 ACTC' ::.: ACAC'	750 TTCTTCTT::::::::
540 550 560 600 TACTATGCCTTGCGGCGGCAGGTTTCCGAGTCTCCCGGAAGTTTGCCATGTTCATCACCTTGTCC ::::::::::::::::::::::::::::::::::	610 CAGATCACT-CAGATG ::::: :::::: CAGAT-TCTGCAGATG	680 TGTCACTCTCACTT :: ::.: :: TGCCACACA-ACAA. 690 700	750 760 770 780 790 CCATTTCTTCTTTGAGGCCTACATCGGCAAAATGAGGAAAACAAC-GAAAGCTGAA :::::::::::::::::::::::::::::::::::
540 550 600 I400 TACTATGCCTTGCGGCGGCGGCTTTCCGAGTCTCCCGGAAGTTTGCCATGTTCATCACCTTGTCC ::::::::::::::::::::::::::::::::::	610 620 630 640 650 660 670 I400 CAGATCACT-CAGATGCTGATGGCTTTAACTACCTGGTCTTCTGCTGGATGCAGCATGACCAG :::::::::::::::::::::::::::::::::	680 690 700 710 720 730 740 I400 TGTCACTCTCACATTTCAGAACATCTTCTGGTCCTCACTCATGTACCTCAGCTACCTTGTGCTCTTCTG ::::::::::::::::::::::::	
I4 CIG	I4 CIG	I4 CIG	1400 CIG30

Fig. 180

20	40	60	80 240	100	120 360	140 420	145
Y TAC	G GGT	L TTG	I ATC	D GAC	S AGC	A GCG	
W TGG	ტ ტტტ	A GCC	Q CAG	H CAT	L	K AAA	
H CAC	A GCT	YTAC	S TCC	Q CAG	Y TAC	K AAG	
L CTG	V GTA	Y TAC	Γ	M ATG	M ATG	V GTG	
F TTC	M ATG	S	T ACG	W TGG	L	K AAA	
I ATC	D GAC	Y TAC	I ATC	N AAC	S TCA	g ggC	
$_{ m L}$	K AAA	M ATG	F TTC	F TTC	S TCC	I ATC	
K AAG	Y TAC	V GTC	M ATG	V GTC	M	$^{ m Y}$	
Q CAG	S	A GCC	A GCC	L CTG	F TTC	A GCC	
K AAG	Y TAC	H	F TTT	Y TAC	I ATC	E GAG	
R AGG	W	V GTA	K AAG	N AAC	N AAC	F TTT	
L	S TCT	G GGC	R CGG	IATT	Q CAG	F	
I ATT	Y TAC	Y TAT	S TCC	V GTC	F TTT	F TTC	
I ATC	L CTG	N AAC	V GTC	C TGT	H	H CAT	
$ ext{F}$	L	M ATG	R CGG	GGC	S TCC	C TGC	
I ATA	V GTG	TACT	F	M ATG	m Y	F TTC	*
T ACG	TACT	M ATG	G GGT	L CTĠ	C TGC	L	団
D GAT	I ATC	F	A GCG	M ATG	Q CAG	L CTG	Ą
GGT	H	W	A GCT	Q CAG	D GAC	L	×
L CTA	H	G	R GGG	TACT	N AAT	Y TAC	H

Fig. 18P

ACG AAG GCC GAG TAG

TGTCAGAGCTGAGGAGGAAGACATAGCTCAGGGTCATCACGAAAAATAATAGACAAAAAAAA
CATATGGTGCAGCTAAAACAAAACATTATGAGCAGACGCTAAGCCCAAGGCAGCTTGGGAGTGAAGATTAGGTT
GTAAGTTTATGATCCTTTTTGGGTGAGGACTCACTGAGAACACTGCTGCTGAGGGACCCCCTTCCCTTTACCTGTCAA
CTCTAGAACACACTAGAAGCCAAGGCAGCCATGGGCAAGGAGATTAGTGGACAGCAAGCA
GGGAGATCTATTCAGAGTTTTTTTTTTTTTTTTTTTTTT
TGTGAGCACACCCACGCGCATGCAGACACCCCACCTACACACTATCTGCAGATGACCAGTGTCCTATGCTGTTTTTAC
AAATAAAACTTGAGACAAGAAAAAAAAAAAAAAAAAAAA

Fig. 180

DOFERIO DITER

	10	20	30	40	50	09	70
human murine rat	human MNMSVLTLQEYEFEKQ urinerat rat	KQFNENEAIQWM:	FNENEAIQWMQENWKKSFLFSALYAAFIFGGRHLMNKRAKFELRKPLVLWSLTL 	SALYAAFIFG 	GRHLMNKRAK 	FELRKPLVLW	SLTL
human murine rat	human AVFSIFGALRTGAYMVYILMTKGLKQSVCDQGFYNGPVSKFWAYAFVLSKAPELGDTIFIILRKQKLIFL urine	MVYILMTKGLKÇ LKÇ	TKGLKQSVCDQGFYNGPVSKFWAYAFVLSKAPELGDTIFIILRKQKLIFL LKQSVCDQSFYNGPVSKFWAYAFVLSKAPELGDTIFIILRKQKLIFL LGDTIFIILRKQKLIFL	OVSKFWAYAF OVSKFWAYAF	CDQGFYNGPVSKFWAYAFVLSKAPELGDTIFIILRKQKLIFL CDQSFYNGPVSKFWAYAFVLSKAPELGDTIFIILRKQKLIFL 	TIFIILRKQK TIFIILRKQK TIFIILRKQK	CIFL CIFL CIFL
human murine	human HWYHHITVLLYSWYSYKDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQITQMLMGC murine HWYHHITVLLYSWYSYKDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSOITOMLMGC	SYKDMVAGGGWE	KDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQITQMLMGC KDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSOITOMLMGC	AYSYYALRAA AYSYYALRAA	GFRVSRKFAM GFRVSRKFAM	FITLSQITQM FITLSOITOM	LMGC LMGC

rat HWYHHITVLLYSWYSYKDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQITQMLMGC human VVNYLVFCWMQHD--QCHSHFQNIFWSSLMYLSYLVLFCHFFFEAYIGKMRKTTKAE murine VINYLVFNWMQHDNDQCYSHFQNIFWSSLMYLSYLVLFCHFFFEAYIGKVKKATKAE

Fig. 18R

rat VINYLVFNWMQHDNDQCYSHFQNIFWSSLMYLSYLLLFCHFFFEAYIGKVKKATKAE

FINTER OFFER

79	158	5 229	25 289	45 349	65 409	85 469	105 529	125 589
CGTC	STGA	מז	GGT	L CTA	D GAC	$_{ m TTC}$	F	9 9
366C	3AGG(V G GTG	E GAG	$_{ m CTG}$	A GCG	L CTC	V GTC	L
GTAG(AGAA(I I I	S TCC	D GAC	T ACT	P	9 9	A GCG
GAGA	GAGC	W C TGG	D GAC	A GCC	A GCT	A GCG	R CGC	R CGG
ACCG	ACTA	T G ACC	P	A GCT (A GCC	$_{ m L}$	GGT	$_{ m L}$
GGGA	TCGC	M C AT	TACC	C TGC	P CCT	W TGG	L CTG	TACG
ACCT	CATG	້ວອວວ	9	I ATC	L TTA	G GGC	A GCG	N AAC
CACA	CACC	GTCG	L TTA	C TGT	E GAG	PCCC	D GAT	S TCT
GCCT	GTGC	GGTG	G GGG	K AAA	A GCC	R CGC	L CTA	S TCA
CACC	TCCG	CCCT	V GTT	$^{ m Y}$	P CCA	L	E	L
9229	GCCA	CTGT	R CGC	P CCC	V GTG	R CGC	N AAC	D GAT
GAGT	AAGG	TGTA	$_{ m CTG}$	C	DGAC	Q CAG	H CAC	CIC
CTAA	CGGC	CCTC	M ATG	N AAC	Q CAG	L	D GAC	L CTG
GCGG	TCCT	AGCT	C TGC	H CAC	L	A GCG	L CTA	R AGG
GAGC	IGCC	ACAG.	L	L	ე მმმ	N AAC	H CAC	L CTG
CGGG	5005	CTGC	L CTG	A GCG	L CTA	H CAC	L CTG	9 9
CGIC	ACCC	CAAC	T ACA	R CGT	GGC	S AGC	A GCC	S AGC
CACG	AAGA	ACTG		P	T ACT	L CTG	R CGC	A GCC
GTCGACCCACGCGTCCGGGGAGCGCGCGTAAGAGTGCCGCACCGCCTCACAACCTGGGAACCGGAGAGTAGGGGCCGTC	GGCTGGCAAGAACCCGCCGTGCCTCCTCGGCAAGGGCCCATCCGGTGCCACCCATGTCGCACTAGAGCAGAAGAGGGGTGA	M GTCCTGAACTGCAACCTGCACAGAGCTGCTCTGTACTGTCCCTGGTGGTCGCCGCC ATG	$_{ m CTG}$	P	C TGC	D GAC	L CTG	N AAC
GTC	255	GTC	L	F	S AGC	L	Q CAG	V GTC

Fig. 19A

145 649	165 709	185 769	205 829	225 889	245 949	265 1009	285 1069
$_{ m L}$	G GGC	L CTG	A GCG	C TGC	F	Q CAG	E GAA
CGC	L CTG	H CAC	A GCC	D GAC	D GAC	$_{ m TTC}$	P CCG
N AAC	Y TAC	T ACC	$_{ m CTG}$	C TGC	R CGC	FTTC	R CGG
N AAT	L	A GCC	E GAG	P CCT	V GTG	R CGC	K AAG
$_{ m F}$	H CAT	S AGC	P CCT	$rac{ ext{L}}{ ext{TTG}}$	A GCC	V GTG	L CTA
L CTG	S AGC	L CTG	V GTA	P CCT	S AGC	R CGC	ე ეე
CIT	L	G GGT	S TCC	N AAC	$_{ m CTG}$	S TCC	L CTT
$_{ m CTG}$	A GCG	H CAC	I ATC	N AAC	0 0 0 0	A GCG	A GCT
K AAG	R CGC	$_{ m CTG}$	H CAC	H CAC	R CGG	PCCC	P CCA
E GAG	L CTG	H CAC	G GGA	$_{ m ITG}$	Q CAG	V GTA	A GCC
$_{ m CTG}$	9 66C	D GAC	L CTG	$^{ m Y}$	H CAC	K AAG	S TCG
A GCG	H CAC	F	R CGG	L	\overline{W}	F	S TCG
	${ m F}$	S TCC	N AAC	g GGC	R CGC	A GCC	C TCC
L	A GCC	F	S TCC	N AAC	Q CAG	$_{ m ITG}$	N AAC
ი ცვმ	H CAT	s TCG	S TCC	K AAG	L CTA	C TGC	E GAG
D GAC	E GAG	A GCC	CIC	L	$_{ m CTG}$	V GTA	F TTT
L	D GAC	L CTC	D GAC	FTC	H CAC	Y TAC	V GTC
D GAC	$_{ m L}$	E GAA	L CTG	A GCC	Y TAC	E GAG	R CGC
H CAC	H CAC	N AAC	T ACT	P	L	R CGC	s AGC
CGC	V GTG	C	L	L	R CGC	A GCG	CAC

Fig. 19B

325 1189 345 1249 365 1309 385 1369 405 1429 ഗ ര P CCG Q CAG P CCA R CGC H CAC F TTC P PCCC V GTC S TCC E GAG T ACG G GGC A GCC Q CAG A GCA Q CAG Q CAG TACC S AGC GGA TACA $_{
m TTC}$ D GAC T ACC V GTA N AAC N AAC L CTG N AAC PCCA PCCA N AAC A GCG N AAC H CAC FTTC Y TAC PCCG P CCA C TGC H CAC R AGG GGC A GCT L A GCC T ACA YTAC L CIC I ATA L E GAG L CTG L CTG T ACC L PCCC A GCC V GTG S AGC LCTT R CGC P R AGG E GAG L TTG P E GAG L P L Γ V GTA P CCA V GTG L CTG Q CAG S AGC ĞĞĞ TACT S TCA Q CAG L P S TCC GGC R CGC R CGG D GAC A GCC P CCG G GGC PCCG C TGC STCC $_{\rm CTG}$ V GTG K AAG GGT S TCG A GCC F TTT A GCC A GCC V GTG H CAC H V GTT L C IGC R CGT Γ W TGG VGTG V GTG V GTG $_{\rm TGT}^{\rm C}$ GGC P A GCG GGC E GAG A GCG FITC S AGC CA GCC L V GTG YTAC I ATT I ATC L CTG C TGC A GCT L S AGC GGA N AAC L CTG R CGC R AGA 7 CGC PCCA H CAC M ATG GGC A GCG $\overset{Y}{\text{TAC}}$ T ACA $_{\rm TGC}^{\rm C}$ E GAG E GAG TACC CCC A GCT A GCC D GAT H

Fig. 19(

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S P Q G Q A S T S T * AGC CCG CAA GCG TCC ACA AGC ACG TAG	45 158;
	166
CTGGAGGCCTGCAGCTGAAGGCTGGCTCTGAGTCCGCCAGCTCCATAGGCTCCGAGGGTCCCCATGACAACCTAGACTGC	174
CAGGGCTCCCCCACCCAGGCCCCCCACCCTCTTGCTGCTCGCCCTGCTTCGGTTCCAGAGAACTGGCAGATACT	181
GGTGGGAAGCACTGTGCCTGGCCCCCCAGCTTCCTGTATGGGCCTCGAAACACAATGGGCCTTCTCGCTCACTGGTAGA	1898
GACAGGGGTTGTGGTCCCCAACCTGCCTTCTGCCCCTGCACAGGACCCAAAGGCCCCCAGGCCCTGCAAGGTGTG	197
CTAGTTCCTGCTTTCCCGGGGACTTCCTAGTGCCCAAATGCCCTGTGAGGCTGAGAGCCCAGGCCCCTGTGGCTTTCA	205
ACACAGCACAGCTGTGGAAGTGGCTGTGTTCTTCTACAGCCTGTGGAAGAACCCCTGTAGCAGAGCCTCCCATCCACCC	213
TCAGGGGCTGAGGCAGCTCTCGAGGAGTGGTGGTCAAGAGCTGACGCCAGGGCCACCTCCCCTTCCCAAGGGGGGTGGGAG	221
GGAGTGGGCCCACAGGGAAAAAAAAGGGGGCTCTGAAGGAAG	2293
CCGCCCTCTGGTGAAATGGGACTCCCTCCATCCACCAACCCCAACCTCCTGAAAGCTTCACAACTTCACGGGAGTCC	2372
GGTGGCAGGCACCAGGCAGGAAAGGCTCCTCAAGAGGTTCCTGGTCTGGCCTAAGCCCCAGCCAAGAGGCCTTGCTC	2451

Fig. 19I

norcata, natan

2895	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
2846	CTGGGGGCCCCCCATGGCCATCCTGGACCTCGCTGCTCCAGAGTTTAATAAAGGTAGCACATGCTTATTGCTAGAAAAA 2846
2767	CTTCATATGCATCTCACTGCTCCCACTGCAGGGGGGGGGAAGGGGGGGTCTGGGAGCCCTTCATGTGTGGGGGGCCGAG 2767
2688	GAACTCCACGTCCCTCGAGAGCAGGGCTCTTAAGGGCTGGCACTGGTCTCAGCCTAATGGCTGAGGCGGTACCCTGG 2688
2609	ATGGCCTGCACCCCTGCTTTTCAGCAGTAAAAAGCCCGAAAAGCCTGGCGAGCATGGCCGAGCTGGGAGGGCCGAGCCG
2530	TCTCTGGCCTGGGGCATCCACCCGTTGTTCTGAAGGCAGAGCCCATTCTGTGGGCTCACAAGACACAGTGAAGGGGGATC 2530

Fig. 19]

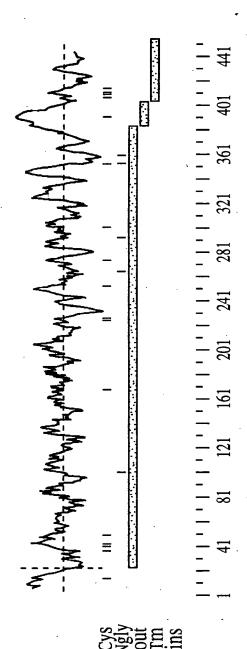


FIG. 19F

10 20 30 40 50 60 70 TLIGTLLCMLRVGLGTPDSEGFPPRALHNCPYKCICAADLLSCTGLGLQDVPAELPAATADLDLSH : : : : : : : : : : : : : : : : : : :	80 90 100 110 120 130 NALQRLRPGWLAPLFQLRALHLDHNELDALGRGVFVNASGLRLLDLSSNTLRALGRHDL-DGLGA: .: .: .: .: .: .: .: .: .: .: .:	140 150 160 200 HLEKLLLFNNRLVHLD-EHAFHGLRALSHLYLGCNELASFSFDHLHGLSATHLLTLDLSSNRLGHISV :::::::::::::::::::::::::::::::::::	210 220 230 240 250 260 PELAALPAFLKN-GLYLHNNPLPCDCRLYHLLQRWHQRGLSAVRDFAREYVCLAFKVPASRVRFFQH .:.: : :: : : : :
10 H MTWLVLLGTLLCMLR : : : : : : : : : : : : : : : : : : :	80	140	210
	H NALQRLRPGWLAPLF'	HLEKLLLFNN	H PELAALPAFLKN-GL
	:	:::::	:::: :::
	P AGVHLVLQGLQSPTC'	P QCHLEKLQLEYC	P CQLETLRLENCGL
	70 80	140	200

Fig. 19C

270 310 320 H SRVFENCSSA-PALGLKRPEEHLYALVGRSLRLYCNTSV-PAMRIAWVSPQQELLRAPGSRDGSI: .: .: .: .: .: .: .: .: .: .: .: .:	340 350 360 370 380 390 SLAIGNVQEQHAGLFVCLATGPRLHHNQTHEYNVSVHFPRPEPEAFNTGFTTLLGCAVGLVLVL : .: .: .: .: .: .: .: .: .: .: .: .: .:	400 410 420 430 440 450 H LYLFAPPCRCCRRACPLPPLAPNTQPAPRAEPHK-SSVLSTTPPDAPSPQGQASTST : :: :: :: : : : : : : : : : : : : : :
270 28 H SRVFENCSSA-PAL: .: .: P DITASGCRDLCRVL	330 340 H AVLADGSLAIGNVQE . : : .: P MLTQNKHLLEL	400 410 H LYLFAPPCRCCRRA : : P LRELDLSNNCVGDP 400 4

Fig. 19F

4 8	96	144	192	240	288	336
c ctg cgg g Leu Arg 15	c cct gag e Pro Glu 0	g cac aac 1 His Asn	g cgc tgg g Arg Trp	g tac aca u Tyr Thr 80	t gag cac e Glu His 95	c tta gag y Leu Glu 0
acc cg Thr Ar	tcc at Ser Il	tac ctg Tyr Leu 45	ctc cg Leu Ar	cgc ga Arg Gl	ttt tt Phe Ph	cca gg Pro Gl
ggg tta Gly Leu	cat atc His Ile	agg ctc Arg Leu	cac ctg His Leu 60	ttt gaa Phe Glu 75	gtg cgc Val Arg	gca gct Ala Ala
ggt ctg Gly Leu 10	ctg aaa Leu Lys 25	aag aac Lys Asn	ctc tac Leu Tyr	cat gat His Asp	tcc cga Ser Arg 90	gtg gct Val Ala 105
ttg cac Leu His	aac tgg Asn Trp	tat ctc Tyr Leu 40	tgc agc Cys Ser 55	gcc ctg Ala Leu	tca gag Ser Glu	tgc tct Cys Ser
aac cac Asn His 5	tcc tcc Ser Ser	cca act Pro Thr	tgt gac Cys Asp	ctg agt Leu Ser 70	aag gtg Lys Val 85	aag aac Lys Asn
ctc ttt Leu Phe	ac ctc sp Leu 20	ca ctg la Leu 35	tg ccc eu Pro	gg ggc rg Gly	tc ttt al Phe	tc ttc al Phe 100
ccg ttt c Pro Phe L 1	act ctg g Thr Leu A	ttg gct g Leu Ala A	aac ccg c Asn Pro L 50	cac cag c His Gln A 65	tgc ttg g Cys Leu V	agc cgg g Ser Arg V

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384	432	480	528	576	624	672
						ς.
ctc Leu	ccg Pro	gct Ala 160	cac His	aac Asn	cca Pro	ggc Gly
agg Arg	tcc Ser	atc Ile	cag Gln 175	cac His	gag Glu	gtg Val
ctg Leu	gtc Val	agc Ser	gag Glu	cac His 190	ccc Pro	att Ile
tcc Ser 125	tgg Trp	ggt Gly	caa Gln	ctg Leu	cgc Arg 205	tgt Cys
cag Gln	gcc Ala 140	gat Asp	gtg Val	cgc Arg	gct Ala	ggc Gly 220
ggc Gly	gtg Val	cag Gln 155	agg Arg	ccc Pro	aag Lys	ctg Leu
gtg Val	cgg Arg	tct Ser	ggc Gly 170	999 Gly	caa Gln	ctg Leu
cag Gln	act Thr	gcc Ala	ata Ile	agt Ser 185	gtg Val	acc Thr
gcg Ala 120	gcc Ala	cca Pro	gcc Ala	gcc Ala	agt Ser 200	acc Thr
cac His	cct Pro 135	gcg Ala	tta Leu	ctg Leu	gtg Val	ttt Phe 215
ctg Leu	gtg Val	gtg Val 150	agc Ser	tgc Cys	aat Asn	ggc Gly
cag Gln	agt Ser	ctt Leu	ggc Gly 165	gtg Val	tac Tyr	aca Thr
gag Glu	acc Thr	ctg Leu	gat Asp	ttt Phe 180	gag Glu	aac Asn
gaa Glu 115	aac Asn	gag Glu	gct Ala	gtc Val	ctt Leu 195	ttc Phe
cct Pro	tgc Cys 130	aat Asn	ttg Leu	ggc Gly	aca Thr	act Thr 210
ctg Leu	ttc Phe	aag Lys 145	gtg Val	gca Ala	cag Gln	gag Glu

DOFFOIT OFFOIT

720	768	816	864	912	096
tgc Cys 240	gca Ala	act Thr	gtg Val	ctc Leu	ctc Leu 320
ggc Gly	cgg Arg 255	agc Ser	cat His	cag Gln	caa Gln
cgt Arg	CCC Pro	ctt Leu 270	aag Lys	gtg Val	ttg Leu
tgt Cys	tgg Trp	atg Met	cac His 285	cgt Arg	ggc Gly
ccc Pro	tgc Cys	tcc Ser	gtc Val	99c Gly 300	atg Met
cca Pro 235	cgt Arg	tcc Ser	agt Ser	aat Asn	ccc Pro 315
gca Ala	aac Asn 250	cag Gln	gcc Ala	ctc Leu	aac Asn
ttt Phe	cgc Arg	gca Ala 265	aag Lys	ggc Gly	tgc Cys
ttg Leu	tgc Cys	agc Ser	cgc Arg 280	aag Lys	ctg Leu
tac Tyr	gcc Ala	ctg Leu	agc Ser	aag Lys 295	gat Asp
ctc Leu 230	cgg Arg	gag Glu	CCC Pro	ggc Gly	tcc Ser 310
ttg Leu	cag Gln 245	cag Gln	gca Ala	ccg Pro	gac Asp
gtg Val	tgt Cys	ctc Leu 260	gat Asp	gag Glu	cca Pro
ctg Leu	tgc Cys	cca Pro	cca Pro 275	ctg Leu	cct Pro
gtg Val	cac His	agt Ser	cca Pro	ttc Phe 290	gta Val
ctg Leu 225	tgt Cys	tcc Ser	acg Thr	gtc Val	gca Ala 305

Fig. 19K

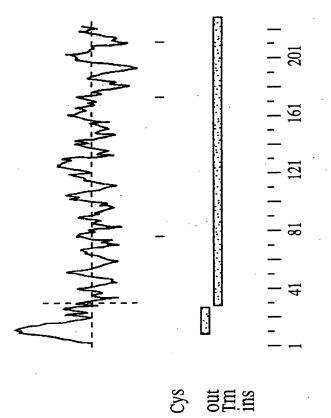


FIG. 191

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Σ	7	PFLFNHLHGLGLTRLRTLDLSSNWLKHISI	30
н	151	.	200
Σ	31	PELAALPTYLKNRLYLHNNPLPCDCSLYHLLRRWHQRGLSALHDFEREYT	80
Н	201	:	250
Σ	81	CLVFKVSESRVRFFEHSRVFKNCSVAAAPGLELPEEQLHAQVGQSLRLFC	130
н	251		300
Σ	131	NTSVPATRVAWVSPKNELLVAPASQDGSIAVLADGSLAIGRVQEQHAGVF	180
н	301		350
Σ	181	. VCLASGPRLHHNQTLEYNVSVQKARPEPETFNTGFTTLLGCIVGLVLVLL	230
H	351	VCLATGPRLHHNQTHEYNVSVHFPRPEPEAFNTGFTTLLGCAVGLVLVLL	400
Σ	231	SCCHCCORACRNRCWPRASSPLQELSA.	279
ж	401	YLFAPPCRCCRRACPLPPLAPNTQPAPRAEPHKSSVLSTTPPDAPS	446
Σ	280	RKASVHKHVVFLEPGKKGLNGRVQLAVPPDSDLCNPMGLQL 320	
II	447	447 POGOASTST455	

Fig. 19M

10	30 129	50 189	70	90 309	110 369	130 429	150 489
L CIG	N AAT	Q CAG	C	L	N AAC	L	GCC
FTTC	D GAC	L CTC	R CGA	L	L CTG	9 990	CIA
CIG	A GCG	F	CIC	PCCT	A GCT	T ACT	I ATC
Q CAG	W TGG	P	CIC	N AAC	V GTG	F	ი ი ი
Y TAC	K AAA	H CAT	$^{ m Y}$	F TTC	Y TAT	I ATA	CIG
K AAG	A GCA	Q CAG	F TTC	P	M ATG	I ATC	¥ TGG
TACC	S TCG	F TTC	A GCC	Q CAG	L	V GTG	Q CAG
W TGG	L CIC	S AGC	A GCT	Q CAG	S AGC	A GCA	S AGC
A GCC	T ACG	H CAC	L CTG	P	T ACC	G GGT	Γ
M ATG	N AAC	E GAG	C TGC	D GAC	GGG	R CGG	V GTG
GAC	I ATC	K AAG	S	V GTA	T ACA	$_{ m L}$	$_{ m CIG}$
CGCC	S	S AGC	F TTC	S AGC	M ATG	M ATG	R AGG
CGT	9 66C	GGG	E GAA	S TCC	D GAC	Q CAG	ი გ
CCCAC	TACC	G GGA	G GGA	D GAC	$_{ m TGT}$	F TTC	ი ი ი
3AAC(V GTT	C TGT	L CIG	S TCA	L	S AGC	L CTG
2992	L	9	$_{ m TTC}$	Q CAA	A GCG	S TCC	F TTC
CGTC	M ATG	E GAG	M ATG	GGG	P CCA	A GCC	G G G C C
CACG	L	A GCC	0 0	A GCA	P	S AGT	V GTG
GTCGACCCACGCGTCCGGCGAACCCCCAGCGTCCGCCGAC	GGG	M ATG	V GTG	A GCT	$_{ m CTG}$	T ACC	S TCG
GTC	A GCC	F	A GCA	R AGA	$_{ m F}$	M ATG	F TTC

Fig. 20A

210 669 250 789 230 290 M ATG V GTT R CGG L TTG I ATC TACC L N AAC A GCC L CTG PCCC A GCA I ATC P CCA V GTG D GAT 9 96C S AGC L CTG Q CAG H CAC $_{\rm CTG}$ E GAG $_{\rm CTG}$ $_{\rm CTG}$ S AGC K AAG A GCC VGTG Γ $_{
m L}$ L CTG E GAA L CTG M ATG K AAG N AAT $_{\rm L}$ TACA A GCA A GCA L CTG IATC GGG T ACC H CAC S TCC VGTG IATC K AAA L R CGT A GCC V GTC L Y TAC S AGC D GAC I ATC PCCT I ATT V GTC I ATC L CTG V GTC V GTG N AAC L V GTT $_{
m L}$ D GAC G GGA P GGC $_{
m TTC}$ \mathbf{F} $\mathbf{T}\mathbf{T}$ G GGG K AAG S AGC Q CAG A GCA G GGC TACA E GAG FTT F TTC Q CAG FTTC I ATC L S TCC GGC N AAC E GAG S AGC V GTG G GGC GGC V GTG L F TTC E V GTG E GAG A GCC Q CAG FTTC S AGC M ATG P C TGC A GCC TACT L GGC IATC I ATT I ATC RCGC V GTT S AGC A GCA S AGC

Fig. 20B

T 330 ACT 1029	L 350 CTG 1089	A 370 GCC 1149	372 1155	SAA 1234	CAC 1313	CTC 1392	AGCTCTCTGGACCCCTCCTACAGCACTAGAGCTAAATCATGAAGTTGAATTGTAGGAATTTACCACCGTAGTGTATCTG 1471	1518
9	P CCC	D GAT (SGTTCCCTGGAGGCTTCTACTGCCACCCGGGTGCTCCTTCTCCCTGAGACTGAGGCCCACACAGGCTGGTGGGCCCCGAA	IGCCCTATCCCCAAGGCCTCACCCTGTCCCCTGCAGAACCCCCAGGGCAGCTGCTGCTGCCACAGAAGATAACAACAC	CAAGTCCTCTTTTTCTCACTACCACCTGCAGGGTGGTGTTACCCAGCCCCCACAAGCCTGAGTGCAGTGGCAGACCTC	GTAT(
F L I L L I G TTC CTC ATA CTC CTT ATA GGC	G R GGC CGG	P I N D CCC ATC AAT GAT		STGGG	AGATA	STGGC	STAGI	
CII	G GGC	I ATC		3CTG(CAGAA	rgcac	CACC	
L	S R FTCC AGG	P		ACAGO	SCCA	rgag1	FTAC	
I ATA	S TCC	L G G T R T CTG GGT GGC ACC		CCACA	rgcī	4GCC1	SAATI	
CIC	L CTG	R CGC		SAGG	CAGCI	CACAZ	STAGO	
F TTC	G R L GGC CGC CTG	T ACC		SACTO	}GGG(מכככ	AATTC	
9 9	G . G	GGC		CTGAC	CCCC	CAG	3TTG2	CGGC
Q I L CAG ATC CTT	L L CTG CTG	G GGT		TCC	SAACO	rtacc	rgaa(3000
I ATC	L CTG	L CTG		CTT	rgcac	3GTG:	ATCA:	AAGGG
	P CCG (CIG		rgcī	וכככי	3GGT(CTAA	aaaai
L CTG	R CGH	R AGA		3666.	מממנ	rgca(4GAG(AAAA!
A GCA	H	E GAG		CACC	CTGT	CACCI	CACTA	AAAA
F H TTC CAT	L CTA	E Q GAG CAG		TGC	CACC	CTAC	ACAGO	ATAA1
F TTC	GGG CTA	E GAG		CTAC	SCCT	CTCAC	CCT	ratc?
A GCC	N AAT	S AGC		3GCT.	SAAGO	rttt(מממנ	AGAT
E A GAG GCC	A L Y N SCC CTC TAC AAT	A E E S SCA GAG GAG AGC		rggac	וכככנ	CTCT	rggac	AATCATAAACTAGATTATCATAAAAAAAAAAAAAAAAAA
W IGG	L	E GAG	* TGA	וכככו	CTA	AGTC(rctci	CATA
9 3,60 1	A 3CC	A 3CA	S AGC .	3GT.	ופכנ	CCA	AGC.	AAT(

Fig. 20(

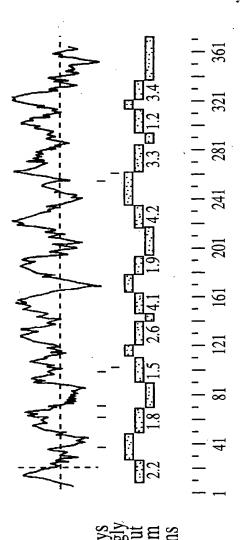


FIG. 20L

72	25 132	45 192	65 252	85 312	105 372	125 432	145 492
W TGG	W TGG	FTC	L CIG	G GGA	N AAC	L	CIC
H V CAC TC	$\overline{\mathtt{W}}$	R CGG	L CTT	Q CAA	K AAG	H CAC	A GCC
P F	V GTG	R CGG	GGG	L CTG	GGG	S TCC	A GCT
A 1 GCC C(E GAG	V GTA	T ACT	E GAG	K AAA	A GCC	S AGT
	A GCT	V GTA	P	L CTG	Q CAG	N AAT	V GTG
M GCGTGCGCC ATG	ტ ტტტ	T ACG	E GAG	A GCC	I ATC	Y TAC	V GTC
ופכפנ	I ATT	A GCC	T ACG	E GAG	$^{\mathrm{C}}$	P	$^{ m Y}$
36067	GGC	$^{ m L}$	$_{ m CTG}$	M ATG	E GAG	Q CAG	T ACC
SCGGG	L CTG	E. GAG	T ACG	S AGC	T ACT	L CIG	C TGC
4GAG(9 990	G GGG	L CTG	F TTC	K AAG	F TTC	K AAG
3CTC2	W TGG	S	T ACA	A GCC	K AAG	R CGC	P CCC
rgaa(L CTG	S TCT	L CTG	FTTT	E GAG	IATC	Q CAG
36001	R AGG	V GTG	$_{ m TTC}$	L CTG	V GTG	F	F TTC
AGCTO	A GCA	T ACA	D GAC	A GCC	P CCC	N AAC	A GCC
GTCGACCCACGCGTCCGCGGGACAGCTG	A GCA	K AAG	Q CAG	E GAG	A GCC	F TTC	Y TAC
gece	L CTG	R CGT	I ATC	R CGA	E GAG	C	T ACC
GTC	$_{ m CTG}$	P CCG	9 66C	A GCC	W TGG	E GAG	9 99 9
SACGO	W TGG	V GTG	T ACC	GGC	S	T ACC	C TGT
BACCC	V GTC	L	Q CAG	V GTG	IATC	Q CAG	V GTC
GICC	A GCT	N AAC	S TCC	Y TAC	A GCG	N AAC	$^{ m Y}$

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Fig. 21A

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165 552	185 612	205	225 732	244 789	8 6 8	947	1026	1105
295 GGC	C	T ACC	T ACA		CTT	GTG		
$_{ m TGT}$	T ACA	M ATG	S TCA	* TGA	CGAACCTCACTTTGTAGGCTCTGCCTATGTACCTGAGAGTGTGGGCAGCTT	AGGTO	CTG	SACAC
G GGA	R AGA	PCCT	H CAC	P T T P CCC ACC ACT CCA	rgTG(3AGC?	CGTT(3CAG(
R CGT	L	A S V GCA AGT GTC	P CCA	T ACT	AGAG	IGCC	4CCA(CCT
TACT	S V TCT GTC	S AGT	C T R TGT ACT CGG	T ACC	CTG	3CTA	3TGG2	CACAC
W TG(S TCT	A GCA	T ACT	P CCC	rgta	SACTO	3GAA(3ATG
L	CIC	ж б	$_{ m TGT}$	9	CTA	STCC	SAGAC	4GGC(
$_{ m CTT}$	S TCT	G GGA A	S AGC	V T W C GTA ACA TGG	rcTG	rggac	CTG	CTGCA
L T CTC ACC	I T ATC ACC	M AT	V GTG	T ACA	4GGCT	3CAG1	3GAC(CAG
L	I ATC	K AAG	M ATG	V GTA	rTGT?	3066	SCAC	rcaa(
L CIC	L	S L ; AGT TTG	W TGG	L S C TTA TCC TGC	CACT	3GGA(366C	ract:
A GCC	L	S AGT	L	S TCC	ACCT	rTCA(rggg(GCTC
PCCC	H CAT	E GAG	F	L TTA	ACGA	CTTC	SATA	3GCA(
CCC	K AAG	M ATG	A GCC	P CCA	CTCA	ACTT(366C	AACT
Q CAG	L CTT	S AGC	L CIG	N AAC	rTGG(3TCT?	3CAA(ZCCG
CCC	A GCC	W TGG	A M GCC ATG	R CGG	CCTT	CAAG(3TCT(CTGC
$_{ m TGT}$	S P AGC CCT	L		A GCA	CTGG(4CGA(CCGT	IGCT(
R CGG		S TCA	R AGG	W TGG	3TAC(3ACG	rggc(3GCA!
PCCT	Q CAG	PCCT	L CTA	T S W A ACT TCC TGG GCA	AGACAGAGTACCTGGCCTTTTGGCTCAA	CACGGGGGACGACGACAAGGTCTACTTCTTCAGGGAGCGGGCAGTGGAGTCCGACTGCTATGCCGAGCAGGTGGTG	GCTCGTGTGGCCCGTGTCTGCAAGGGCGATATGGGGGGGCGCACGGACCCTGCAGAGGAAGTGGACCACGTTCCTGAAGG	CGCGGCTGGCATGCTCTGCCCCGAACTGGCAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGACACCTC
L CTA	P CCA	S TCA	Q CAG	T ACT	AGA(CAC	GCT(SCC

DOPEDIED DETENT

1184 1263 1579 1658 1737 ACCCTGTACCCAGGCCCTGGTTGTGATGGCTGCCCAGCCCCGCCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAG CTGGCACACACCACCTTCTTTGGGGTTTTTCAAGCACAGTGGGGTGACATGTACCTGTCGGCCATCTGTGAGTACCAG TTGGAAGAGATCCAGCGGGTGTTTGAGGGCCCCTATAAGGAGTACCATGAGGAAGCCCAGAAGTGGGACCGCTACACTG GGGCCCCGCGCTGCTGCTGAAGGCTACCTTGTGGCTGTCGTGGCAGGCCCGTCGGTGACCTTGGAGGCCCGGGCCCCCC ATTGCGCCGGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAGGCTACTGAGAGGACCTTGGTGTACCCCCTGGAGCTG CCCAAGGAGCCCACCAGTCCCCCCTTCCGGCCCTGTCCTGAACCAGATGAGAAACTTTGGGATCCTGTCGGTTACTACT ATTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCCCGGTGCCAGCCCGGTGGGGGGGCCCCCTTCGCCACCTCCAGG TGCAGCAACGCCAGCCACTGCCCGACTCCAACCCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGTCGGCGGA

Fig. 21(

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2811	GTCCCCGCGTATTTTTTTGAATATTTTGAGATTTTTTATATTGA
2764	AGAGGGTGGGCCTGCTGTGGACAATGGCATACTCTTCCAGCCCTAGGAGGAGGGGCTCCTAACAGTGTAACTTATTGT
2685	GCCCCGGGGTTCAGTGTTTTTATACTTGCCTTCTTCCTGTACAGGGCTGGGAAAGGCTGTGTGAGGGGAGAAGGG
2606	TGAATGTTTTCAGGGTGGGGGGGGGAGGTGGAGCCTCCTGTGTGTTTGGGGGGGAAGGGTGGGT
2527	AGGTGGGGTGGACAGGGTGCTGTGCCCCTTCAGAGGGAGTGCAGGGCTTGGGGGTGGGCCTAGTCCTGCTCCTAGGGCTG
2448	CTATGAAGGGGAAGGGGTCGTATCACTTTGTCTCCTACCCCCCACTGCCCCGAGTGTCGGGCAGCGATGTACATATGG
2369	GCGTGCGCGCTTGTGGCATAGCCTTCCTGTTTCTGTCAAGTCTTCCCTTGGCCTGGGTCCTCCTGGTGAGTCATTGGAG
2290	TCAAGGCAGAAGTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTG
2211	CAGGGCACCAGCCTCGCAGAAGGCATCTTCCTCCTCTGTGAATCACAGACACGCGGGACCCCCAGCCGCCAAAACTTT
2132	GACAGATACTGCCCAGCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACTGCCACTTGGTGTGGCTCAC 2132

Fig. 21I

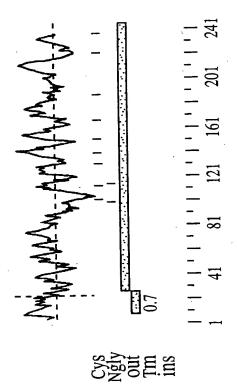


FIG. 21E

First of the caret

Σ H	10 MAPHWAVWLLAAGLW ::::::::::::::::::::::::::::::::::::	GLGIGAEMWNLVPRKTVSSGELVTVVRRFSQTGIQDF::::::::::::::::::::::::::::::::::::	30 .VPRKTVSSGE: .::::::::::: .VPRKTVSSGE: 30	40 LVTVVRRFSQ: :.:::::: LATVVRRFSQ: 40	1 1 1 1	0 60 70 IQDFLTLTEHSGLLYVGAR ::::::::::::::::::::::::::::::::::::	70 .a. .: AR 70
Σ H	80 EALFAFSVEALELQG ::::::::::: EALFAFSMEALELQG 80	90 ISWEAPAEKKI ::::::::: ISWEAPVEKKT 90	100 ECTQKGKSNQ' ::.:::: ECIQKGKNNQ' 100	110 TECFNFIRFL ::::::::::::::::::::::::::::::::::::	120 QPYNSSHLYV :::::::: QPYNASHLYV 120	90 100 110 120 130 140 AISWEAPAEKKIECTQKGKSNQTECFNFIRFLQPYNSSHLYVCGTYAFQPKCTYI ::::::::::::::::::::::::::::::::::::	140 TYI ::. TYV 140
Σ	150 160 170 180 190 200 NMLTFTLDRAEFEDGKGKCPYDPAKGHTGLLVDGELYSATLNNFLGTEPVILRYMGTHHSIKTEY	160 GKCPYDPAKGH	170 ITGLLVDGELY	180 SATLNNFLGT	190 EPVILRYMGT	ĨΑ	210 FWL
田							!
E H	220 NEPHFVGSAFVPESVG ::.: VSAALLP	230 SFTGDDDKIYF 	240 FFSERAVEYD: :	250 CYSEQVVARV 	260 ARVCKGDMGG	230 270 280 GSFTGDDDKIYFFFSERAVEYDCYSEQVVARVARVCKGDMGGARTLQKKWTTFLK :	280 FLK
Σ \mathbb{H}	290 ARLVCSAPDWKVYFNQ : : CPQPP	300 LKAVHTLRGAS :.:: ALLTL	310 WHNTTFFGVF	320 QARWGDMDLS : L-	330 AVCEYQLEQI 	300 340 350 QLKAVHTLRGASWHNTTFFGVFQARWGDMDLSAVCEYQLEQIQQVFEGPYKEYSE :::: ALLTL	S E E

Fig. 211

		710	720	730	740	750	. 091	770
Σ	M ASERTLVYPLELPK	YPLELPKEP	ASPPFRPGPE	STDEKLWDPVG	YYYSDGSLKI	VPGHARCQPG	EPASPPFRPGPETDEKLWDPVGYYYSDGSLKIVPGHARCQPGGGPPSPPGIPGQP	3QP
				••			•••	
H	1 1 1		1 1 1 1 1 1 1	M			GPTTP	-
							240	
		780	790	800	810	820	830	
Σ	M LPSPTRLHLGGGRN		IANGYVRLQLO	SNANGYVRLQLGGEDRGGSGHPLPELADELRRKLQQRQPLPDSNPEESSV	LPELADELRR	KLQQRQPLPD	SNPEESSV	

Fig. 21H

420 TNF TS.	490 SRS • • • • • • • • • • • • • • • • • • •	560 KVR 	630 CYS	700 GAK
4 KKNT : T	490 FAGSRS	H I	PYRC	7 LEKG.
PLLV ::. -LLI	KKVL	CNQY	RHSG	고 요 고 고
410 RLGR	480 TLSQS: 	550 TSKM	620 AAQS	690 LRRR.
)QVKE	480 PVESLVLSQS::: SMESLKMGRA	7ANLE	TLVVP	TATE
400 PLMEI	470 DQEPV	540 LVQHV	610 TGLQ?	680 CLVLLI :
370 380 390 400 410 420 RPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPLLVKKNTNF .: :: :: :: :: :: :: :: :: :: :: :: :: :	440 450 460 470 480 490 YTVLFIGTGDGWLLKAVSLGPWIHMVEELQVFDQEPVESLVLSQSKKVLFAGSRS :::::::::::::::::::::::::::::::::::	530 540 550 CVATTSGRSGSFLVQHVANLDTSKMCNQYG .:::	580 620 630 630 610 620 630 LPCHLSSNLAHAHWTFGSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRCYS :	650 660 670 680 690 700 VVAGSSVTLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLREELEKGAK ::::ARNPLSCVT230
O T I I I I I I I I I I I I I I I I I I	0 -	0 TSGR .: TS	0 QPGS 	O VVAL
390 LPDNT:	460 FPWIHM:	20 530 WNVNTSRCVATTS:::::::::::::::::::::::::::::::::::	600 LPAEQ	670 VWLAV
TSSLE	450 LLKAVSLGPW .::.: VLRTCSPSLW	NTSF	768QF	INLGI
380 DNGYT	450 WLLK2 .:.	510 520 CVDCVLARDPYCAWNVNTSR : : :: ::	590 AHWTI :	660 EARAPLE :::: -ARNPLS
NWHR.	TGDG	RDPY	NLAH.	TLEAR :: AR 230
370 GSCINN .: .	440 VLFIG	510 DCVLA :	580 CHLSS	650 AGSSV
	4 \TYTV 			
) DPVPS	SLDGA	CTKYF	GTDI	SYLV
360 WARYTD: ::: WTR	430 DRVPG:	500 SLADC' :: -LA	570 ITVVS(640 RLAAE:
360 M QAQKWARYTDPVPSP: ::: HWTR	430 THVVADRVPGLDGAT [*] S	500 QLVQLSLADCTKYRF :: .:: : QLRAM-LAF	570 SIPKNITVVSGTDLV	640 EEQGTRLAAESYLVA'
O I E E	M T H S	Ø ·· Ø	S I	ы Ы п

Fig. 21G

king king king hing kana king

Σ Ξ	1 GGCACGAGG : : GTC	10 GTGGCCGG : . : : GACC	20 3AGTCAA2	3 ACGCGAG : . : : -CACG	30 GGGCAGCG :: CG	40 .GCGCCAGGGATT :::	50 GGAGCTGCACGA ::: CGCG-	60 AAGA(70 GGCTGCTG ::::::: GGACAGCTG
Σ \mathbb{H}	8 GACTGAAGT : :::: GCCTGAAGC 30	80 TTTAGACC : ::: : CTCAGAGC 40	90 CTGGGT(:::: CGGGGC(100 GTCTGCCA :: ::: GTGCGCCA	0 ATGGCCC :::::: ATGGCCC 60	110 :cacacrggg :::::::: :cacacrggg	120 CTGTCTGGCT ::::::: CTGTCTGGCT	80 100 110 120 130 140 GACTGAAGTTTAGACCCTGGGTGTCTGCCATGGCCCCACACCTGGGCTGTTGGCTGCTGGCAGCAGGGCT : :::::::::::::::::::::::::::::::::::	140 GGGCT .:::
Σ Η ΄΄	150 GTGGGGCCTGGGCAT ::::::::::: GTGGGGCCTGGGCAT 100	50 1GGGCATC :::::: 1GGGCATT 110	160 :GGGGCT(:::::	170 GAGATGTG(::::::: GAGGTGTG(0 GGTGGAA :::::: GGTGGAA	180 .ccttgtgcc .:::::::: .ccttgtgcc	190 CCGGAAGACA(:::::: GCGTAAGACA(150	150 160 170 180 190 200 210 GTGGGGCCTGGGCTGAGATGTGGTGGAACCTTGTGCCCCGGAAGACAGTATCTTCTGGGGAG ::::::::::::::::::::::::::::::::	210 GGGAG ::::: GGGAG
Σ Ι΄	220 CTGGTCACAG' ::::::::::::::::::::::::::::::::::::	20 AGTAGTGA ::::: GGTAGTAC 180	230 AGGCGGT :::::: AGCGGT	240 TCTCCCAG; ::::::: TCTCCCAG;	0 GACAGGC ::::::: GACCGGC	250 ATCCAGGAC' :::::::: ATCCAGGAC' 210	260 TTCCTGACAC' :::::::: TTCCTGACAC' 220	220 230 240 250 260 270 280 280 280 280 280 280 280 280 280 28	280 AGAAC .::.: GGAGC
Z H '	290 I ATTCTGGCCT' :::::::: CCACTGGGCT' 240	90 ::::::::::::::::::::::::::::::::::::	300 ATGTGGGG ::::: ACGTGGGC	310 GGCCCGAG :::::: CGCCCGAG	310 GCCCGAGAGGCGC :::::::::: GCCCGAGAGGCCC	320 :TGTTTGCCT ::::::::::::::::::::::::::::	320 330 3 CTGTTTGCCTTCAGTGTAGAGGC :::::::::::::::::::::::::::::::::::	290 340 350 ATTCTGGCCTTTTATATGTGGGGCCCGAGAGGCGCTGTTTGCCTTCAGTGTAGAGGCTCTGGAGCTGCTGCA .:::::::::::::::::::::::::::::::::::	350 CTGCA ::::

420 CAG ::: CAG	0 H H	560 .GGA	30 	700 CCA
42 ACCZ ACCZ	45 CACC :::	G.A.	630 CTGTAC :	7(CTC(
4GCA : . : : 4ACA)	30.66 : :: 31.66	\TTT	3AGC	ACCA :: AC
410 GAAGA(::::: GAAGA	480 GTCTG(:::: GTCTG' 440	550 CAGA! : C	620 .cggT(:: .cg	690 ACCCAC ::::
4 AGGG AGGG	TATG :::: TACG	55 CGTGCA :::: -GTGC-	620 GGACGG :: CG-	690 ATGGGGACCCAC:::: ATGTGG-CCCAC
0 CAGAA ::::: CAGAA 360	0 ATCTG: : : ACCTG	3ACC	TGT	ATGG::
370 380 400 400 420 GGAGGCTCCAGCTGAAAATTGAATGTACCCAGAAAGGGAAGAGCAACCAG :::::::::::::::	440 450 460 470 480 490 TTCATCCGCTTCCTTCAGCCATACAATTCCTCCCATCTGTATGTCTGCGGCACCT ::::::::::::::::::::::::::::::::::	510 520 530 540 550 AGTGCACCTACATCACATGCTCACGTTCACCTTGGACCGTGCAGAATTT ::::::::::::::::::::::::::::::::	580 620 620 cccatatgacccagctaagggtcacaccggactccttgtggacggtgaggress::::::::::::::::::::::::::::::::::	650 660 670 680 690 700 AACTICCIGGGCACAGAGCCGGTIAICCTICGATACATGGGGACCCACCACTCCA::::::::::::::::::::::::::::::::::
TGTA :::: TGTA	CCTC	CACC	ccggacrcc :::::::: ccagccccc	TTCG
0 TGAA :::. TGAG 350	0 AATT ::: AATG 420	GTT	0 CACC :: C C - CC) ATCC
390 AATT :::	460 TACAZ :::: TACAZ	530 TCAC	600 GTCAC.:::GTC-C	670 GTTA
AGAA :::: AGAA	GCC.≱ ::: GCCC	ATGC	AGGG	
380 TGAGA :::: GGAGA 340	50 TTCA : :: TGCA 410	520 :TCAAC ::. :TCG	590 AGCTAAGG : :: .: ACCTCGGT 500	660 CTGGGCACAGAGC :::::::: CTGGACTCGTGG- 540
38 GCT(:	11CCT	510 520 AGTGCACCTACATCAA :::::::::: AGTGCACCTACGTCG- 470	55 CCCA(:: : CCTA(6(GCA(.:.
TCCA :: CCCC	CGCI :::: CGCI	CCTA:::CCTA	TGAC:	CTGG
370 .AGGCT .AGGCC 330	440 CATCC ::::: CATCC 400	510 TGCAC ::::: TGCAC	580 CCCATA: ::: CCCT	650 AACTTC: :: TTCT
.::: .:::	ACTTC .:::	CAAG:	TGCCC TGCCC TGCCC	65 ATAACT :: TTCT 530
TCTT:::TCCT	TCAA :::: TCAA 90	10 :AGCCC :::::: :AGCCC	AAATG(:: TG(TCAA : CC
360 AGGAGCGATCTCTTG ::::::::::::: AGGAGCGATCTCTTG 320	430 ACCGAATGCTTCAAC:::::::: ACCGAGTGCTTCAAC' 80 390	500 ATGCCTTCCAGCCCA : ::::::::: ACGCCTTCCAGCCCA 50	570 570 TGGGAAGGGTAAATG	640 TCAGCCACACTCAAT. ::::::: CCT-CCTCACCC
AGCC:::	GAAT ::· GAGT		GAA(:: -CCZ
AGG ::: AGG 310	::: ACC 380	4	1	
Σ H	Σ H	Z H	Σ Ή	Σ H ·

Fig. 21J

Σ	710 M TCAAGACAGAGTACCI	720 rggcttttgg	720 730 740 750 760 770 TGCCTTTGTAGCCTCTGCCTTTGTGAGGAG	740 CCCACTITGIP	750 AGGCTCTGCC	760 TTTGTCCCTG	770 AGAG
H	::: AGAGCCC 560	CTGCCCTTAAGC 570		::::::: ATCTCCTCATCAC- 580	:::: CTCTCTC 590	:::: :::::::::::::::::::::::::::::::::	::: AGA-
Σ Ξ	780 TGTGGGAAGCTTCACC	790 3GGAGACGATG	790 800 810 840 GGGAGACGATGACAAGATCTTCTTCTTCAGTGAGCGGGCAGTGGAGTATGAC ::::::::::::::::::::::::::::::::::::	800 810 820 ACAAGATCTACTTCTTCAGTGAGCG :::::::::::::::::::::::::::::::::	820 AGTGAGCGGG .: ::: TG-GAGCA 630	830 CAGTGGAGTATGA .: .:::::: -TGGAGGTTTGA 640	840 TGAC ::: TGA-
Σ \mathbb{H}	850 TGCTATTCCGAGCAGG ::.	860 GTGGTGGCTCG .::: ATGGG	860 870 880 890 900 910 GTGGTGGCTCGTGTGGGGGGGGGGGGGGGCGCGCGCGCG	880 GTCTGTAAGGG ::: GTC	890 TGACATGGG	900 GGGAGCACGGACGC : :: :: : CTATGACCC	910 GACGC ::: : GACCC
Σ Н	920 TGCAGAAGAAATGGA .::: AGCTAAGGGCCATGC 680	930 CGACGTTCCTGA :.: :: :: TGGCCTTCTTGT 90	940 AGGCTCGG1 :::: -GGATGGTG	950 TTGGTGTGCTCAGCC .: :::::::: GAGCTGTACTCGGCC 710	960 GCCCCTGACT ::::::::: GCCACACT	70 GAAGG	980 TCTACTT ::: -CAACAA 730
Б Н	990 CAACCAGCTGAAGGC :::: CTTCCTGGGC	1000 GGTGCACACCC	1010 1020 1030 CCTGCGGGGCGCCTCTTGGCACACACACACACACACACAC	1020 CTCTTGGCACA :.::: CA-TTATC	1030 AACACCACCT	1040 1050 CCTTCTTCGGGGTTTTT :::::	1050 TTTT :

Fig. 211

1120 CAAGTGT	1190 GTACCCAG ::: .: GTAGG	1260 ACTGCCG :: .: ACGAC 880	1330 GGCCGCC	1400 GATGGTGC .:: :: -GTGTGGC
1110 AACAGATCCAG : ::: CTCCA-	1180 ACTGACCCGG :::::	1250 12 STTCCCTGGAACTGC : :::: :: CGGGGGACGAC	1320 GCCTCGGTTG : ::. STC-CGA	1390 CCAGGGCTTG
1100 :::: ACCA780	160 1170 1180 GAAGTGGGCCCGCTATACTGACCCGGTA:::::::::::::::::::::::::::::::::::	1240 GGCTACACCA(:::::::::::::::::::::::::::::::	1310 AGGACCAGGTGAAGCCTCGG :::::::::::: -GGGCAGTGGAGTC-CGA 10	1380 GACAGGGTCC :: TC- 950
1090 TTTGTGAGTA : A	1160 CCAGAAGTGG ::: CTTTTGG	1230 1240 CGAGACAATGGCTACACCA(::::::.:: -GAGT-GTGGGCAGCTTCA(860	1300 1310 1320 1330 CTGATGGAGGACCAGGTGAAGCCTCGGTTGGGCCGCC :::::::::::	1370 :::::::: :GTGGTGGCC
1070 1080 1090 1100 1110 1120 GATATGGACCTGTCTGCAGTTTGTGAGTACCAGTTGGAACAGATCCAGCAAGTGT :::::::::::::::::::::::::::::::::	1140 1150 1160 1170 1180 1190 AGGAGTACAGTGACCCAGAAGTGGGCCCGCTATACTGACCCGGTACCCAG :::::::::::::::::::::::::::::::::	1210 1220 1230 1240 1250 1260 GTGTATCAACAACTGGCACCGAGACAATGGCTACACCAGTTCCCTGGAACTGCCG :::::::::::::::::::::::::::::::::	90 ACCCC	1350 1360 1370 1380 1390 1400 AGAACACTAACTTCACACGTGGTGGCCGACAGGGTCCCAGGGCTTGATGGTGC: :: :: :: :: :: :: :: :: :: :: :: ::
1070 SATATGGACC' :: CC	1140 4GGAGTACAG ::::: GAGTAC 800	1210 3TGTATCAAC :::::	1280 1290 TTCATCAAGAAGCACCC(:::::::::::::::::::::::::::	1350 AGAACACTAA
1060 CAAGCGCGATGGGGC ::::::: CATGGGGC	1130 TTGAGGGTCCCTACA ::::::::	1200 CCCTCGGCCTGGTTC : ::::: CTCTGCCTA	1270 GACAACACCCTCAAC ::::	1340 CCCTACTTGTGAAGA ::::: CTGCTA
E H	Z H	Σ H	Σ H	至 田

Fig. 21I

40 CA: CA	0 0 0	90 . 90 30 . 90	750 .TGT ::.
15, AG(- G(16. AC(168 1167 117,	1750 ATGT ::-
AG .:	 	TIG TI	1 AGA ''
0 I : 0	444 G	360 ::	CAAC
0 GT G	0 ACZ : A		0 TTC .:.
53 3CT 3CG	09 09 09 09 09 09	67 CA ::	1740 CACT : : . C-CAC
GTC : :	AC.:	CAC :::: CAC	1740 GACACTICA :.: :::: GGC-CATCT 1170
Ē.	.: ::	: : : : : : : : : : : : : : : : : : :	Ð
0 1 C C C C C C C C C C C C C C C C C C	3GC 3GC - 3C	0 I I	0 ACT .: IC-
52 AA(::	59 1 1	661 AT(:	1730 CGAA(:
3GA		1 3GA :: 3GC 110	1 TGGC::::
 G	D . H	CT CT CT CT CT CT CT CT CT CT CT CT CT C	GT(GTZ)
CC :: 0 :: 0 :: 0 :: 0 :: 0 :: 0 :: 0 :) 4GC : LAC		720 1730 AACATGTGGCGAAC .:::::::::::::::::::::::::::::::::::
51(AG(TT(58(TC/ TC/	65(TG:	1720 CAAC
1 1999 1999 1999	1 3GT 3-C	1 !AC	1 [CC]
CCI	CTC:::	CTJ CT-	1710 1720 1730 1740 1750 ccrrrcaaagargr :::::::::::::::::::::::::::::::
) :: :: -GA	.: GG	ACC) [CT] 11
500 TTT 101	570 CTC ::	64(GGZ :. GAC	1700 1710 CGCTCGGGGTCCTTT :::::: -GCACAGTGG
1 31G:::	1 5CT 3AA	1 'AG' '3AG' 1	
AGG 	300 300 300 100	000	1700 CGCTCGGGGT :::::: -GCACAGTGG
9			. :
490 4CI 1	560 360 .:-	630 1770 277	1700 :GCTCGG :::::
1, GAZ GAZ		1 1 1 0 0 0	1. GTCG(: G(1140
3AG ::: 3AG	LTG 	CTG :- 1	3GT 11
11G(CT::	GA(: :	GT(
180 166	550 3CT 3CT	520 5TA	1690 ACCA(
14 CAT :: CA-	15 GTC -:: 104	16 GTC	16 CA(-TJ
CA 10	AG.	i i	AC T-
ATC	AGP	TTT .: ATG	1690 M GCCACCACCAGTGGT : .::. H GTTTTTCAA
M H	Σ H	Σ H	Σ Ξ
	1480 1490 1500 1 ATCCACATGGTGGAGGAACTGCAGGTGTTTGACCAGG ::::::::::::::::::::::::::::::::	1480 1500 1510 1520 1530 ATCCACATGGAGAACTGCAGGTGTTTGACCAGGAGCCAGTGGAAAGTCTGGTGCTGTCTCAG :::::::::::::::::::::::::::::::::::	1480

Fig. 21M

1820 CAGACCT	1890 CCTGCCT ::CCA	1960 CAGTCCC ::: :: CAGCCCC	2030 ACCTTGT :::::: ACCTTGT 370	2100 TCGTGTGG : ::::: TGGTGTGG
1790 1800 1810 182 TTCCCAAGAACATCACGTTGTGTCAGGCACAGACC :::::::::::::::::::::::::::	1840 1850 1860 1870 1880 CCTCTCGTCCAATTTGGCCCATGCCCACTGGACCTTCGGAAGCCAGGA :::::::::::::::::::::::::::	1900 1910 1920 1930 1940 1950 1960 GCAGAACAACCTGGCTCCTTTCTTTATGACACGGGACTCCAGGCGCTGGTGGTGATGGCCGCACAGTCCC : ::: ::: ::: ::: ::: ::: ::: ::: ::	1970 1980 2000 2010 2020 2030 GTCACTCTGGACCTATCGTTGCTATTCAGAGGAGGAGGAGGACTGGCTGCAGAAAGCTACCTTGT : :: ::::::::::::::::::::::::::::::	2040 2050 2060 2070 2080 2090 2100 TGCTGTCGTCGCTCGTCGTCACTCGAGGCACGGCTCCCTTGGAAAACCTGGGGCTCGTGTGG :::::::::::::::::::::::
1810 ACATCACCGTTGTGTCAGG :: :: :: ::: -CAGCGGGTGTTTGAGG 1200	1870 CTGGACCTTCGG . :: ::	1940 SCTGGTGGTG ::::::::::::::::::::::::::::::	2010 MGACTGGCTG ::::::::::::::::::::::::::::::::	2080 CCTTGGAAAA :::::::::::::::::::::::::::::::
1790 CCCAAGAACA::	1860 ATGCCCACTC .:.:: GTACCAT	1930 ACTCCAGGCC ::::::	2000 CAGGGGACAA ::::::: CAGGGGGGGG	2070 CACGGGCTCCCT : :::::: CCCGGGCCCCCC
1780 .AGATCTATT :::: AGATC	1850 1860 rccaattrggcccargccc ::::::::::	1920 TGACACGGG; ::::::	1990 TCAGAGGAG(:::::::::::::::::::::::::::::::	050 2060 2070 CGTCGGTGACGCACGGGCTCCCCCCCCCCCCCCCCCCCC
1770 1780 TTAAAAAGTCAGATCTA ::: :::: AAGAGATC	1840 CTCTCGTCCA ::.	1910 TCCTTTCTTTA : : :: TACACT	1980 TCGTTGCTAT : . : : : : : : : CCACTGCTTT	2050 TCGTCGGTGA :::::::: CCGTCGGTGA
-	1830 1 ACCCTGCCACC ::: GCC	1900 .caaccrggcrc .::: ::: :ggaccgcra	1970 1 CTGGACCCTAT : ::::::::::::::::::::::::::::::::::	2040 CGTGGCCGGCT ::::::: CGTGGCAGGCC
1760 1 GTAACCAGTATGGCA ::: :::: ::: 1 GTA-CCAGT-TGG	GGTCCT		1970 M GTCACTCTGGACCCT :::::::: H GCCATGCCGGGGCCT 1310	
ΣΗ	Σ Ξ	Σ \mathbb{H}	<u> </u>	Σ H

Fig. 21N

Σ Ξ	2110 CTCGCTGTGGTGGC :: :: :::::: CTGGCGGTGGTGGC	$0 \cdot 0 \cdot 0 = 0$	2130 GCTGTGTGC :::::::: GCTGTGTGC	30 GCCTGGT :::::: GCCTGGT	2120 2130 2140 2150 TGGGGGCTGTGCCTGGTGCTGCTGGTC ::::::::::::::::::::::::::::::::::::	2120 2130 2140 2150 2160 2170 CTGGGGGCTGTGTGCTGCTGCTGCTCCTATCGCTCCGCCGGCGAC ::::::::::::::::::::::::::::	2160 CTATCGCTCCGG ::.::::: CTGTCATTGCGG	2170 ccGGCGAC :::::: ccGGCGGC
Σ H	2180 2230 2240 TTCGAGAAGAGCTAGAAAAGGGTGCCAAGGCATCTGAGAGGACACTGGTGTACCCCTTGGAACTGCCCAA : ::::::::::::::::::::::::::::::::	2190 :TAGAAAAGG :::::::::::: :TGGAGAAAG	220 GTGCCAA0 : :::: GGGCCAA0 1540	00 GGCATCTG/ ::::: GGCTACTG/ 1550	2210 :GAGAGGAC :::::::: :GAGAGGAC	2190 2230 2240 AAAAGGGTGCCAAGGCATCTGAGAGGACACTGGTGTACCCCTTGGAACTGCCCAA :::::::::::::::::::::::::::::::::	2230 .ccccTTGGAAG ::::::::::	2240 CTGCCCAA ::::::: CTGCCCAA 1580
Σ π	2250 GGAGCCTGCCAGTCCC ::::::::::::: GGAGCCCACCAGTCCC 1590 1600	2260 :::::::::::::::::::::::::::::::::::	2270 ccgrccrgg :::::: ccgcccrg	70 GGCCCCGA1 : :: :: TGTCCTGA1 1620	2280 SAAACTGAT: :::::: SAACCAGAT:	2260 2300 2310 CCCCTTCCGTCCTGGCCCCGAAACTGAGAAACTTTGGGATCCTGTCGGGTAC ::::::::::::::::::::::::::::::::::::	2300 TGGGATCCTG::::::::::::::::::::::::::::::	2310 TCGGGTAC ::::::: TCGGTTAC 1650
Σ Ξ	2320 TACTATTCGGATGGC :::::::::::::: TACTATTCAGATGGC 1660 167	67 67	2340 AAGATTGTG(::::::: AAGATAGTA(40 TGCCTGG::::: TACCTGG	2350 STCACGCCC::::::::::::::::::::::::::::::::	2330 2340 2350 2360 2370 2380 TCTCTCAAGATTGTGCCTGGTCACGCCCGGTGCCCAGCCTGGGGGTGGGCCCCCTT :::::::::::::::::::	2370 23 :GGGGGTGGGCCCCC :::::::::::::::::::::::	2380 3CCCCCTT ::::::: 3CCCCCTT
Σ Ξ	2390 CCCCACCTCCTGGCA : ::::::::::: CGCCACCTCCAGGCA 1730 174	2400 GCATACCTG ::::::::: GCATCCCAG	24. GCCAGCC: ::::::: GCCAGCCI	10 TCTGCCTT(::::::TCTGCCTT(2420 :TCTCCAAC: ::::::::::::::::::::::::::::	2400 2410 2420 2430 2440 2450 TACCTGGCCAGCCTCTCCCAACTCGGCTCCACCTAGGAGGTGGTCGGAA : :::::::::::::::::::::::::::::::::	2440 .cctaggaggres:::::::::::::::::::::::::::::::::::	2450 GGTCGGAA ::::: GGGCGGAA 1790

Fig. 210

2470 2480 2500 2510 2520 TTATGTGCGTTTACAGTTGGCCGGAGGACCCGAGGATCTGGGCCACCCAC	2540 2550 2560 2570 2580 2590 GAATTACGACGGAAACTACAACAGCGCCAGCCGCTGCCTGACTCCAACCCAGAGG :::::::::::::::::::::::::::	2610 2620 2630 2640 2650 GGGACCCCCCCCCCCCTCATTGGCGGGGGGGGGTCTCATGGGAGGTGCA-CTCTTAA ::::::::::::::::::::::::::::::::	2680 2690 2700 2710 2720 CAGCTACCTCAGGGACATGGCAGGGGCACTTGCTCTGCCTGGGACAGACA	2750 2790 2790 2790 2790 2790 2790 2790 279
2490 2500 TGGGCGAGAGGACCGAGGAGGAT TAGGAGGGGAGGACCGGGGGGGGGG	2560 23 ACAACAGCGCCAGCC .:.::::::::: GCAGCAACGCCAGCCZ	2630 2	2700 TGGCAGGGGCACTTG :::::::::::::::::::::::::::::::::::	2760 2770 AGCATGGGCACTO ::::::::::::::::::::::::::::::::::::
2470 2480 "TATGTGCGTTTACAGT ::::::::::::::::::::::::::::::::::::	2540 2550 AATTACGACGGAAACT ::::::::::::::::::::::::::::::::::	2610 2620 GGACCCCCCACCTCA ::: ::: :: :: GGAACCCCC-ACCGCG	2680 2690 AGCTACCTCAGGGACA::::::::::::::::::::::::	2750 STGAGGACCTGCTC
2460 CTCAAATGCCAATGGTT:::::::::::::::::::::::	2530 CCTGAGCTCGCGGATGA :::::::::::::: CCTGAGCTCGCGGATGA 1870	2600 2610 2620 2630 AGTCTTCAGTATGAGGGACCCCCCCCCCCTCATTGGCGGGGGGGG	2660 2670 M CTTTTGCACAGGCACCA:::::::::::::::::::::::	2730 2740 M CATCATTTGCCCGGCCG ::::::

Fig. 21P

2860 CCAAA ::::	GAA :. TAT	766 	0 ·· 0 0 ·· 0 0 ·· 0	TTTG: .: TCAG
28 AGCC ::: CGCC	rgrg :::: rgrg	0 6 6 6 6 6 6 6 6 6 6 6 7	60 TACC :::: TACC 2410	3130 TTGTACCCCTTT::::: CTGTGCCCCTTC.
	:0 'GCAT' : .: 'GTGT' 2270	2990 CTTG(::::	3060 TCCTA::::::	3130 ACCCC' ::::
2850 ACCCC::::	2920 GTATG ::.:: GTGTG'	11CC 11CC	CTTC :: TCTC	GTTGT:::::
2 5GGA : : : : 5GGA	3TTG ::: 3TTT 50	2980 ACGTC : ::: AAGTC 330	3050 CTTTG ::::: CTTTG	3120 GGGTG ::::: GGGTG
.TGTGG(::: .CGCGG(2910 2920 ATATGTGTTGGTATGCATGTGGAA : :::::::::::::::::::::::::::::::::	298(TCACG: ::::: TCAAG:	3(CACT	31 CAG(::::
2840 GACA' ::::	29 -ATA : :	TCTA:::TCTG	ATAG .:: GTAT 90	AGGA. .:: TGGA. 2460
2830 2840 GTGAATTTGAGACA':::::::::::::::::::::::::::::::::	'GCAT, : ATTTGC, 2250	2970 :TGTC' ::: :TGTT'	3040 GGTC; : :: G-TC(3110 GGGA. :::
0 : AAT: : AAT(00 GTG(GTA:	1) 5 5 5 5 5 5 5 5 5 5 5 5 5 5 7 7 7 7 7	GAAC
2830 -GTGA :::: TGTGA	2900 GTTTG :: :: GTCTG	O ACTI .:: GCCI	0 GGAA :::: GGAA 80	0 CGGGG; :::: TGGAGG
2800 2810 2820 2830 2840 2850 2860 CTTCAGCCTCACAGAGACA-CACCCTCCTCTGTGAATTTGAGACATGTGGGACCCCAGCAGCCAAA : ::::::::::::::::::::::::::::::::	2870 2880 2890 2900 2910 2920 CTTTGCAAGGAAGAGTTTCAAGATGTGGGCGTGTTTGTGCATATATGTGTTGGTATGCATGTGGAA :::::::::::::::::::::::::::::::	40 2950 2950 2960 2970 2980 2990 TGTGTGTGTGTGTTGTTGTAACTTTCCTGTCTCTATCACGTCTTCCCTTGGCCTGG .::::::::::::::::::::::::::::::::::	3010 3020 3030 3040 3050 3060 CTGGTTGAGTCTTTGGAGCTATGAAGGGGAAGGGGGTCATAGCACTTTGCTTCTCCTACC ::::::::::::::::::::::::::::	3090 3100 3110 3120 3130 TGGGGCAGTGATGTACATACGGGGAAGGGACAGGGTGTTGTACCCCTTTTG : ::::::::::::::::::::::::::::::::
2820 -CACCCTCCTCT ::::::: TCTTCCTCCTCT 160 217	2890 TGTGG(::::	TGT:	ATGI	ATGTA(::::::::::::::::::::::::::::::::::
2820 ACCC :::::TTCC	28 GATC :::: GATC	TG :: CTTG	3020 GGAGCT :::::: GGAGCT 2370	3090 AGTGAT :: ::: AGCGAT
28 CA-CA(:: :. CATCT	TCAAG; ::::: TCAAG; 2230	50 TG: 3GCGC' 2300	30 ITGG :::: ITGG	30 3CAG ::::
0 GAGACA .::.:: AAGGCA	2880 GGTT' .::	2950 GTGTG ::::	STCT:	
281(CACAGC ::::: CGCAGZ	GAAGAC:::::	2940 2950 TGTGTGTGTGTGTG ::::::::::::::::::::	3010 TTGAG : ::: T-GAG 2360	3080 .GCTTT .::: .G-TGT
00 CAGCCTCACA ::::::::: CAGCCTCGCA	0 AGGA ::: AGGC	2940 TGTGT(:::::	3 TGGT :::: TGGT	070 3080 CTGTCCCAAGCTT ::: ::::: CTGCCCGAG-TG
2800 TTCAGCCT . ::::: ACCAGCCT	2870 rgcaa : ::: rrcaa	2 3TGT(3TGT(3TCC 3TCC 3CCC
2800 (CTTCA::::::::::::::::::::::::::::::::::	2870 2890 2900 ACTITGCAAGGAAGAGGTTTCAAGATGTGGGCGTGTTTGTGCAT ::::::::::::::::::::::::::::::::::::	AA TG 28	3000 3010 3020 3030 3040 3050 3060 GGTCCTCCTGGTTGAGTCTTTGAGGGGAAGGGGGTCATAGCACTTTGCTTCTCCTACCCC : ::::::::::::::::::::::::::::::::	m U I
M H G·Q	ж н . А	2930 ™ ™ G	∑ H	М Н Н А

Fig. 21Q

COVECTO CTTECT

Σ Ξ	3140 3150 GGGGAGTGCGGGACT ::::::::::: AGGGAGTGCAGGGCT 2490	υ i	3160 :GGGGGTGGGCC' :::::::::::: TGGGGTGGGCC' 2500	3170 TAGCCCTGCT :::::::: TAGTCCTGCT 510	3180 CCTAGGGCTG' :::::::::: CCTAGGGCTG' 520	3190 ;TGAATGTTT ::::::::::::::::::::::::::::::	3160 3170 3180 3190 3200 CGGGGGTGGCCCTAGCCTCCTAGGGCTGTGAATGTTTTCAGGGCGGGGTT :::::::::::::::::::::::::::::	GTT:
Σ Ξ	3210 3220 GGGGGTGGAGATGGA ::::::::: GGGAGATGGA	3220 3AGATGGAACC :::::::::: -AGATGGAGCC 2560	323 :rccrgc' :rccrgrgrg' 2570	0 TTCAGGGGGA(:: .:::: TTTGGGGGGAV	325 3GGTGGGCP .::::::	326 GGGCCTCCC7 ::::::::::::::::::::::::::::::::	3230 3240 3250 3260 3270 ACCTCCTGCTTCAGGGGAGGGGTGGGCAGGGCCTCCCACTTGCCCTCCGGG .:::::::::::::::::::::::::::::::::	9 ·· 9
Σ H	3280 TTCGGTGGTATTT :::::::: TTCAGTGGTATTT 2620 26	30 30	3300 TTGCGCTCTT(:::: :::: TTGCCTTCTT(0 TC-TG-ACAG(:: :: ::: TCCTGTACAG(2650	3310 GGGCTGGGAAG :::::::::: GGGCTGGGAAA	3320 ;GGTTGTTC ::::::	290 3330 TATITGCGCTCTTC-TG-ACAGGGCTGGGAAGGGTTGTTGGGGGAGGGAAGGG ::::::::::::::::::::	უ უ
m Σ π	3340 3350 M AGGAGGTGGGCA ::.:::::: H AGAGGGTGGGCC 2690 2	TGC:::700	3360 3370 TATGGATACTGGCCTAT : : : : : : : : : : : : : : : : : : :	3360 3370 3380 3390 TATGGATACTGGCCTATCCTCTCCCTGCTCTGGGAAAAGGGCT- :.:::::::::::::::::::::::::::::::::::	3380 CCTGCTCTG ::::::: FCCAGCCCTP	3380 CCTGCTCTGGGAAAAGGGCT ::::::::::::::::::::::::::::::::::::	3360 3370 3380 3390 3400 TATGGATACTGGCCTATCCTCTCCCTGCTCTGGGAAAAGGGCTAACAGTGTA :::::::::::::::::::::::::::::::::	F. :
Σ H	3410 34 ACTTATTGTGTCC:::::::::::::::::::::::::::	2007	3430 XTATTTATTT:::::::::::::::::::::::::::::	3430 3440 3450 3460 ACATATTTATTTGTAAATATTTGAGTATTTTATATTGA .:.::::::::::::::::::::::::::::::::::	3450 TTTGAGTATT:::::::::::::::::::::::::::::	3460 TTTATATTG?::::::::::::::::::::::::::::::	3430 3440 3450 3460 3470 ACATATTTATTTGTAAATATTTGAGTATTTTTATATTGACAAATAAAT	¥

Fig. 21R

Fig. 22A

128 588	148 648	168 708	188 768	208 828	227 885	964	1043	1122
L TIG	H CAT	R AGA	S TCT	CCT		SCAC		
F TTT	Q CAA	R AGA	P CCT	Y TAT	* TGA	TGTGTTATTTGATAGGCCGGGCATGGTGGCTCATGCCTGTAATCCCAGCAC	CTGGCCAACATGGTGAAACCCGGTCTCTACTAAAAATTCAAAAATTACCTA	CCTACTTGGGAGGCTGAAGCAGGAGAATTGCTCGAACCTGGGAGGCAGAGG
V GTA	L CTA	F TTC	$_{ m L}$	P CCA	H CAC	AATC	AAAA	GGAG
GGA	R AGG	IATT	G GGA	P CCA		CTGI	TTC	ACCTG
A GCT	N AAT	IATC	A GCA	P CCA		ATG	AAAZ	CGAZ
A GCT	C TGT	S TCC	D G GAT G	S P TCA CCA	CIC	GCTC	ACT	TGCI
I ATT	K AAG	P CC	ЫΚ	တ 🖸	S TCT	GGTC	CTCI	AGAAT
$_{ m L}$	T ACT	T ACT	V T GTG G	V GTT	M ATG	GCAI	ceel	'AGG
GGA	I ATC	H CAC	S TCT	S AGT	S	99009	AAACC	BAAGO
TACT	C TGT	R AGG	P	H CAC		ATAGO	GTG	GCT
CTG	L	GGG	P	K AAA	K AAA	TTTG/	ACATO	3GGA(
L	Y TAT	R AGG	$_{ m L}$	R AGA	FTTT	STTAI	SCCA	ACTTO
g GGC	$^{ m Y}$	E GAA	P CCA	T ACC	V GTA	rtgro	CTG	
M ATG	9 9	Y TAT	S TCT	L	R AGG	AAATI	CAG	וכככז
V GTT	L	V GTC	$_{ m TTG}$	A GCG	F TTT	raag?	SAGAC	STAGI
D GAT	L TTA	A GCC	A GCC	V GTG	GGA	GTAT	STTC	SCCT
I ATA	G GGA	S TCA	A GCT	A GCA	K AAA	rttT(AGGAC	SCAT
K AAA	FTT	S	E GAG	Q CAG	T ACA	STCAI	3GCC7	rggg
E GAG	I ATT	C TGC	E GAG	E GAA	H CAC	CTACCTTGTCATTTTGGTATAAGAAATT	TTTGGGAGGCCAGGAGTTCGAGACCAGC	GGCGTCATGGGGCATGCCTGTAGTCCCA
R AGA	V GTT	P CCA	P CCT	Y TAT	GGG	CTA(TTT(999

Fig. 22F

		TIGACICI 1438	ATAAAGAG 1517	TAAAAAG 1596	CTTTGGGA 1675	CTACAAAA 1754	GAATCGCT 1833	GACTCCAT 1912	CGGGGGGT 1991	GTTAAATT 2070	GTAGTGGG 2149	ATGAAAAG 2228	TGCCCCTG 2307	AAATTTGT 2386	TTAATGTT 2465	2498
		CTTGGACCTGAACTTGATCATTATCAGCTTGATAAGAGACTTTTTGACTCT	TTTTTGTAATGTTTTTAATGGTTCAAAAAAAATCTTTCTT	TCCTTTGTACAGATAAAGGTTATAGATTTCTTGTGTTGAATATAAAAAG	CAGTGGCTCACGCCTGTAATCCCAGCA	CCTGGCCAACATGGCAAAACCCCGTCT	CCAGCTACTGGGGAGGCTGAGGTGGGA	GGCGAGATTGTGCCATTGCACTCCAACCTGGGCGACAGAGTGAGACTCCAT	TCCAAAAAGATATTGGACCTACTCTTTCTTAGGATTTTTTGGCGGGGGGT	CAGTATAAATCTGTGACCTTAATATAATCACTTGGTTTTATATGTTAAATT	AGTTTAGTTCTTAACTCTTGCTGTCAGTCATGTTTTATTATAGGTAGTGGG	CTATTTGCTATGAAGTTAGTTCTTCAGAAGATACAAGTTTGCAATGAAAAG	CTAGGAGACACTAGAACTTAATGAAGT	TCTGTATAACTACATATGATTATTTG	GTGGAAAAAGTAATTTGCTTTTCTGCTCTTAAAATAATATTGATTAATGTT	
GAAGAAGAAGACCACAAAAGACAI GACIAI CCAACIIII I I AI GA		TACTGTACCACAGAAGTTCTGTCTTGGACCTGAACTTG	ATATCCTTGCAGTTAAGAAGAAAGCACTTTTTTTGTAATGTTTGT	CATAGGTAGAATTAGTGAACTCTTTGGATCCTTTGTACAGATAA	CAAGGATGTCTAACCATTAAGATTATCCAAAGTCAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA	GGGATAGGTGGGCGGATCACCTGAGGTCAGGAGTTTGAGACCAĠCCTGGCCAACATGGCAAAAACCCCGTCTCTACAAAA	ATACAAAAGAAATTAGCCAGACATGATGGCGGGTGCCTCTAATCCCAGCTACTGGGGAGGCTGAGGTGGGAAATCGCT	TGAACTCGGGAGGTGGAGGTTGTAGTGAGGCGAGATTGTGCCAT	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TAGAAATACTTCACAGAATTTGACATTTCAGTATAAATCTGTGA	ATTGCACAGCAGTCATCATATTTTGCAGAGTTTAGTTCTTAACT	GTCAGTAGTTTTCTTCTTCTAAAAAATACTATTTGCTATGAAGT	GATTIGCAAGGGTIGTTATGCTATCAAATAAACAGACCTAAAATCTAGGAGACACTAGAACTTAATGAAGTTGCCCCTG	TTACTGATTAGTAAATACTCCCATCTTCGTTGCAAAATTATCTCTCTGTATAACTACATATGATTATTTTGAAATTTGT	TAAACTTCATAAGTAATAGTTTGAGAATGTGGAAAAAAGTAATTT	ACCAGAAAAAAAAAAAAAAAAAGGGGGGGCGGC
	GAAGAAGAAG	TACTGTACCA	ATATCCTTGC	CATAGGTAGA	CAAGGATGTC	GGGATAGGTG	ATACAAAAGA	TGAACTCGGG	CTCAAAAAAA	TAGAAATACT	ATTGCACAGC.	GTCAGTAGTT	GATTTGCAAG	TTACTGATTA	TAAACTTCAT,	ACCAGAAAAA

Fig. 22(

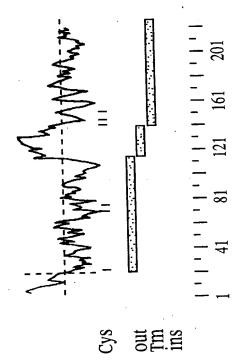


FIG. 22D

60	160	208	256	304	352
GTCGACCCAC GCGTCCGCTG CGTTCTCACC CCTGGACCAC CCTGGGAGAA CAGTTGACCG AAGTTTGTTT GGCAGTTGCT GCTGGACT ATG TTT CTG CTT CTG GTG GTA CTC 113 Met Phe Leu Leu Val Val Leu Leu 15	CAG CTG CCC AGA CTT ACC CTC GCG GTT CCT CAT ACA AGA AGC CTA Gln Leu Pro Arg Leu Thr Leu Ala Val Pro His Thr Arg Ser Leu 10	AAT TCT GAA CAT GCC CCA GAA GGA GTC TTT GCA TCA AAA AAA GCA Asn Ser Glu His Ala Pro Glu Gly Val Phe Ala Ser Lys Lys Ala 30	AGC ATC TTT ATG CAC CGT CGC CTC CTA TAC AAT AGA TTT GAT TTA Ser Ile Phe Met His Arg Arg Leu Leu Tyr Asn Arg Phe Asp Leu 50	CTC TTC ACT CCC GGG AAC CTG GAG AGA GAG TGC TAT GAG GAG TTC Leu Phe Thr Pro Gly Asn Leu Glu Arg Glu Cys Tyr Glu Glu Phe 60	AGT TAT GAA GAA GCC AGA GAG ATC CTC GGG GAC AAC GAA GAA ATG . Ser Tyr Glu Glu Ala Arg Glu Ile Leu Gly Asp Asn Glu Glu Met 75
GT. AA	AGC Ser	AAG Lys 25	GCA Ala	GAA Glu	TGT Cys

OCYSCIEC CILECT

Fig. 22E

400	448	496	544	592	640
A TCA y Ser	: TTA / Leu 120	TAT	A GCT	A ACC 1 Thr	GGA Gly
AGA Arg	GGC Gly	TAC TYr 135	TCA Ser	AGA Arg	GCG Ala
ACA Thr	ACT Thr	GGT Gly	TCT Ser 150	TTC Phe	GAC Asp
ACC Thr	CTG Leu	CTT Leu	GGT Gly	ATT Ile 165	GAG Glu
CCA Pro 100	CTT Leu	TTA Leu	CAA Gln	ATC Ile	TCA Ser 180
GGA Gly	GGC Gly 115	GGC Gly	TAT Tyr	Ser	TCC Ser
AAA Lys	ATG Met	TTT Phe 130	CCA Pro	CCG Pro	TCA Ser
GTC Val	GTT Val	GTT Val	CAG Gln 145	ACA Thr	TCG Ser
TCA Ser	GAT Asp	GTT Val	AGG Arg	CAC His 160	CCA Pro
TAT Tyr 95	ATT Ile	TTG Leu	AAT Asn	AGG Arg	TCT Ser 175
GAA Glu	AAA Lys 110	TTC Phe	TGT Cys	ACC Thr	TTG Leu
CGG Arg	GAG Glu	GTA Val 125	AAG Lys	AGG Arg	GTC Val
TGG Trp	AAA Lys	GGA Gly	ACC Thr 140	AGA Arg	GCT Ala
TTC Phe	AAC Asn	GCT Ala	ATC Ile	ACA Thr 155	GAA Glu
ACA Thr 90	GTC Val	GCG Ala	TGT Cys	\mathtt{TAC}	GAG Glu 170
ATC	GAT Asp 105	ATT Ile	CTG	GTC Val	CAT

Fig. 22F

Fig. 22G

COFEDITO CILIBRA

GAGAAAAGAG	ATGTCAAGAG	SAGAAAAGAG ATGTCAAGAG GTTTTTTGTTT TTTTTTTT AAATTACTAT TTATGGGCCT	${ t TTTTTTTT}$	AAATTACTAT	TTATGGGCCT	1623
CACTTGGAAA	AGTGCTTGCC	CACTIGGAAA AGIGCIIGCC AIGCAAAIAG AAGGACAGGA GIICAAICCI CAIIACCCAC	AAGGACAGGA	GTTCAATCCT	CATTACCCAC	1683
ATTTGAAACA	AATAACAAGA	ATTIGAAACA AATAACAAGA AAAACAAACC AAAAAACCAA AACAAACAAA	AAAAAACCAA	AACAAACAAA	ATCTTGAGAA	1743
CTTGAGTGAA	TACCGGTAAC	CITGAGIGAA TACCGGTAAC CICAGGGCIA GGCACIGIAA CIGAAICAGG AGCCICCAGA	GGCACTGTAA	CTGAATCAGG	AGCCTCCAGA	1803
TCCAGGGAAA	CGCTGTCTCA	CGCTGTCTCA ACAAATAAAT AAATAAGTAA GTCAGTGAGG TGGTCTTTAA	AAATAAGTAA	GTCAGTGAGG	TGGTCTTTAA	1863
ACCCAGCACT	TGAGAGCCAA	TGAGAGCCAA AGGCAGGCAG AGCTCAGTGA GTTGGAGACC AGCCTGGTCT	AGCTCAGTGA	GTTGGAGACC	AGCCIGGICI	1923
ACAAAGCAAG	TTCTAAGGGA	TTCTAAGGGA GCCAGGGCAC AGAGAACCC TGTCTGAAGG AAAAAAAAA	AGAGAAACCC	TGTCTGAAGG	AAAAAAAAA	1983
AAAAAAAA GGCGGCCGC	252255255					2002

 α

Fig. 22H

<

<u>novicientalini</u>

D H	н н	ATGTTTCTGCTTCTGGTGGTACTCAGCCAGCTGCCCAGACTTACCCTCGC 50 	
U D	51	GGTTCCTCATACAAGAAGCCTAAAGAATTCTGAACATGCCCCAGAAG 97	
ם ט	U 80	GAGTCTTTGCATCAAAAAAGCAGCAAGCATCTTTATGCACGTCGCCTC 147	
H	101		
ტ	148	. CTATACAATAGATTTTAGAACTCTTCACTCCGGGGAACCTGGAGAG 197	
H	151		
נ	201		
ם ב	201	AGAGIGCAATGAAGAGITCIGIAGITAIGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAG	

297 347 350 397 400 450 497 497 GGGACAACGAAGAAATGATCACATTCTGGCGGGAATATTCAGTCAAAGGA ITGGTTACTATCTGTGTATCACCAAGTGTAATAGGCAGCCATATCAAGGT CCAACCACAGATCAGATGTCAACAAAGAGAAAATTGATGTTATGGGCCT CCAACCACAAAATCAGATGGCAACAGAGAGAAAATAGATGTTATGGGCCT TCTTCAGCTGTCTACACAAGAAGGACCAGGCACACACCGTCCATCTTT 398 448 451 248 251 298 301 351 401 G G 工 G 田 G 出 G 工 \mathbf{H}

Fig. 22J

<i>(</i> D	498	CAGAACCCATGAGGAAGCTGTCTTGTCTCCATCGTCATCCTCAGAGG 544	4
· 	498	CAGAAGACCTGAGGAGGCTGCCTTGTCTCCATTGCCGCCTTCTGTGGAGG 547	7
<i>(</i> D	545	ACG	4
₩.	548	ATGCAGGATTACCTTCTTATGAACAGGCAGTGGCGCTGACCAGAAAACAC 597	7
(D	595	AGTGTCTCACCACCACCTCCATATCCTGGGCCAGCAAAAGGATTTAGGGT 644	₽ [†]
7	598	AGTGTTTCACCACCACCACCATATCCTGGGCACACAAAAGGATTTAGGGT 647	
ניז	645	ATT	
•••	648		

Fig. 22K

, s ==		MFLLLVVLSQLPRLTLAVPH.TRSLKNSEHAPEGVFASKKAASIFMHRRL 49 - .
	50	LYNRFDLELFTPGNLERECYEEFCSYEEAREILGDNEEMITFWREYSVKG 99
	51	
(D	100	PTTRSDVNKEKIDVMGLLTGLIAAGVFLVVFGLLGYYLCITKCNRQPYQG 149
	101	: :
, D	150	SSAVYTRRTRHTPSIIFRTHEEAVLSP.SSSSEDAGLPSYEQAVALTRKH 198
,	151	
, 5	199	SVSPPPPYPGPAKGFRVFKKSMSLPSH 225
	200	SVSPPPPYPGHTKGFRVFKKSMSLPSH 226

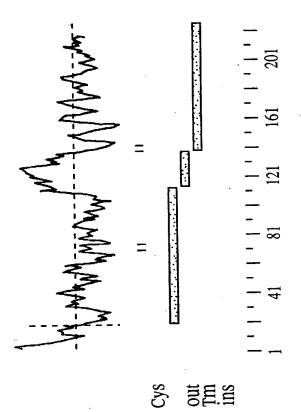


FIG. 22N

79	11 146	31 206	51 266	71 326	91 386	111 446	131 506
GGA	LCTC	C TGC	K AAG	S AGC	N AAT	E GAA	G GGA
ACCI	999	P CCC	K AAG	S TCC	C TGC	S AGC	P CCA
SCAGG	L CIG G	T ACG	A GCA	E GAG	E GAA	K AAG	S TCT
GAGCGGGTGGGCCGGCGGGCCGGAGCACGGCCGCCGCAGGACCTGGA	A GCG (PCCG	T ACC	Y TAC	F TTC	L CTG	C TGC
SCAC	A GCC (KAAG	D GAC	K AAG	D GAC	Q CAG	C TGC
AGCA	R CGG (K AAG	V GTG	S TCC	S AGC	L CTG	V GTG
CCGG	R CGC (A GCC	M ATG	L CTG	S AGC	₩ TGG	K AAA
3AGG(P CCG (A GCC	999	T ACG	E GAG	W TGG	L CTG
CCGG	L CTG (E GAG	Q CAG	K AAG	C TGC	A GCC	T ACA
3066	R CGC (P CCG	N AAC	E GAA	L CTG	E GAG	K AAG
GTGG(M ATG (A GCG	F	E GAG	GGG	L CTG	V GTG
GCGG(מכפככ	Р ССС	K AAG	W TGG	E GAG	H CAC	C TGT
GGGA	ACCC	P CCG	D GAC	A GCT	L	E GAG	F TTT
GGCT	CGCT	L CTG	V GTG	T ACG	I ATC	E GAG	W TGG
2525	GCAG	$_{ m CTG}$	L	N AAC	E GAG	Q CAG	E GAG
BDD5	TCCC	L CTG	999	GGG	Γ	A GCG	$_{ m F}$
CANG	GTCT	L CIG	R	999	L CTG	E	$_{ m L}$
ACGCGTCCGCACANGGCCGGCGCGCGCTGG	GCTCCGGCTGCGTCTTCCCGCAGCGCTAC	L	C TGC	9 9	R GGC	L CTA	D GAC
CGTC	3066	P CCG	R CGG	FTT	I ATT	M ATG	P CCT
ACG	GCT	$_{ m CTG}$	H CAC	N AAC	E GAG	Q CAG	Y TAT

Fig. 23A

				27213	,01		
151	171	191	211	231	251	271	291
566	626	686	746	806	866	926	986
N AAT		E GAG	N AAC	V GTG	N AAC	P CCA	V GTG
G	M	N	TACC	D	A	9	D
GGG	ATG	AAC		GAT	GCC	9	GAT
S	H	R	$_{ m CTG}$	V	N	E	A
AGC	CAC	CGG		GTG	AAC	GAA	GCA
C TGC	C TGC	LCTC	GGC	$^{\mathrm{C}}$	K AAG	GGG	CTGT
CCC	R CGG	S TCG	S TCG	A GCC	$^{\mathrm{C}}$	T ACA	Q CAG
R	C	S	C	9	F	C	G
AGG	TGC	AGC	TGC	9		TGC	GGA
Q	S	F	T	E	Q	9	H
CAG	TCC	TTC	ACG	GAG	CAG	9	CAC
S	GGG	Y TAC	K AAG	D GAC	A GCG	V GTG	E GAG
G	D	g	C	L	A	C	R
GGA	GAC	GGC	TGC	CIG	GCT	TGT	AGG
	g	D	S	VGTG	S	S	A
9	GGC	GAC	TCC		AGC	AGC	GCG
Q	Q	M	E	W	C	S	$_{ m TAC}$
CAG	CAG	ATG	GAG	TGG	HGC	TCC	
C	R	C	D	ე	P	D	9
TGC	AGA	TGC	GAC	ე		GAC	990
A	S	D	$_{\rm TGT}^{\rm C}$	V	P	C	S
GCA	AGC	GAC		GTG	CCT	TGT	TCT
L		T	A	E	P	E	I
	GGG	ACT	GCC	GAA	CCG	GAG	ATC
C	D	C	T	C	E	E	$_{\rm TGT}^{\rm C}$
TGT	GAT	TGC	ACA	TGT	GAG	GAA	
D	G	$_{ m L}$	C	E	A	C	E
GAC	GGA		TGC	GAG	GCC	TGC	GAG
P	S	P	I	299	A	T	K
	AGC	CCG	ATC	880	GCG	ACG	AAA
G	C	g	S	C	C	Y	$_{ m TGT}$
GGT	TGC	GGC	AGC	TGC	TGT	TAC	
Y	H	Q	H	D	E	S	N
TAC	CAC	CAG	CAC	GAC	GAG	TCC	AAC
TACC	ე <u>ე</u> ნ	Y TAC	TACC	R AGA	D GAC	9	G GGA

Fig. 23B

<u>norcolololleol</u>

				2	43/36	1	
311	331 1106	351 1166	354 1175	1254	1333	1412	1432
T ACT	V GTG	E GAA		AGT	TTG	AAA	
N AAT	c TGT	R CGC		CTGC	TTGG	AAAZ	
Y TAC	A GCC	S		TCTC	ATTT	AAAA	
C TGC	D GAT	PCCC		3005	TGCZ	CAAZ	
N AAC	E GAA	L CTG		AGGAT	ACAGO	TAAI	
E GAA	T ACG	Q CAG		CTGZ	TAAZ	STAGG	
N AAC	E GAA	T ACA		16600	נטטטן	ATTG	
K AAA	E GAA (P CCG		ATGI	TTGI	GACC	
R AGG	F TTC	S AGC		GAAZ	TCAI	AATI	
V GTG	9 66C	E GAA		CGTO	SATTC	ATA?	
C TGT	D GAC	G GGA		GTCC	GTTC	TGT	
TACC	P CCT	E GAA		AGGAT	AACG	TCTI	
K AAA	C S TGT C	T ACA		AGA	CTCI	CAGI	
C S L A E K TGC TCA CTA GCA GAA AAA	V GT(A GCC		PATTC	TGC1	GAT	
A GCA	CTGT	E GAA		AAATI	TGCC	TTT	<i>r</i> \
L CTA	V GTC	A GCT		TTT	SAGGC	TAT	AGAC
S TCA	$^{ m Y}$	E GAG		ACCC	GGAG	CTTC	CGCI
	G S Y V GGG AGC TAC GTC	P A E A E A T CCG GCA GAG GCT GAA GCC ACA	* TAA	GTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGT	GACAGCGGGGGGAGAGGCTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTG	TCTTAAACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAAAAAAAA	AAAAGGGGGGGCGGCTAGAC
D E		P CCG	$_{ m CTG}$	35225	AGCC	TAA	\AGGG
D AC	P CA	P CG	D SAC	GTG	GAC	TCI	AAZ

Fig. 23(

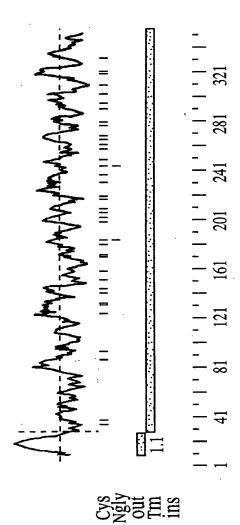


FIG. 23D

YEF YES YES YES YES 140 140 140 150 150 150 150 150 150 150 15	SS SS TL
60 AWEEKSLSKYEF ::::::::: AWEEKTLSKYES 60 70 130 LPGTYGPDCQEC :::::::::::::::: SPGTYGPDCQEC CDESCKTCSGPT CDESCKTCSGLT	SHTA OLP
0 ::::: EEKSI GTYGI GTYGI GTYGI ::::: ESCKI ESCKI	340 GRGKS : GESPJ
60 NTAWEEKS ::::::: 60 130 CCLPGTYG ::::::: CCSPGTYG 130 200 TACDESCK ::::::: TACDESCK 200 270 270 270 270 270 270 270 270 270	RRSG : ATEG 340
SGGN SECT STCT STCT STCT STCT STCT STCT STCT	340 TDSRRRSGRGKSHTATL AEAEATEGESPTQLPSR 340 350
50 TARKNEG : . : : : : 120 MFCVHTL 120 120 130 LRNETHS : : : : : : LRNETHS 260 260 260 ECDSTCV 260 260	330 CCLC-T :
50 NTARK 120 120 EWFCV 120 120 120 120 130 190 190 EECDS EECDS	DRRC DRRC : : EDAC 330
DGMAN SYFS:	
10 20 30 40 50 60	280 330 340 C YSKQKGECADIDECSLETKVCKKENENCYNTPGSFVCVCPEGFEE-DRRCLC-TDSRRRSGRGKSHTA ::::::::::::::::::::::::::::::::::
ALVDK .:::: GLVDK 40 11 QTLKK .:: LCIDCI 110 110 120 120 120 130 130 130 130 130 130 130 13	3 VCVC VCVC 32
DRCR HRCR HRCR HRCP	PGSF:::
30 30 30 30 30 30 30 100 100 170 170 170 170 170 17	310 LETKVCKKENENCYNTPGSF
ASRKPT :: 3 1 LEQHEE 10 10 6SCQCH ::::: GSCRCH CAAETP CAAETP CAAEPP	NENC NENC
ARVA ARVA O O O O O O O O O O O O O O O O O O O	0 CKKE : .
20 LLPPPARVASRK::::::::20 20 90 NDFECNQLLEQH ::::::::::::::::::::::::::::::::::::	300 300 300
 	CSLI
10 C MHLPPAAAVGLL-LL] : : : : : : : : : : 10 10 70 80 C SEIRLLEIMEGLCDSI : : : : : : : : : : : : : : : : : : :	YSKQKGECADIDECS : :.::::: YAREHGQCADVDECS 290 P
10 MHLPPAAAVGLL SE : : : : : : : : : : : : : : : : : : :	2 3ECA :.:: 3QCA 29
LLPPZ ::: ::: ::: :::: ::	SKQK(
C MF 140 C SE C SE C SE C SE C SE C SE H	280 C YS :: H YZ

H EDL

4 4-	75 7	-a -a	7.
0 CCACA ::::: CCGCA	CAC:	$\begin{matrix} \ddots & \ddots & \ddots & \ddots & \ddots & \ddots & \ddots & \ddots & \ddots & \ddots $	0 0 0
50 -CC GCC	0 : 0 0 : 0 0 : 0	180 0180 0180 0180	250 GGCG(:::: GGCG(
ACT.	110 716C	AAT GCC	TIC
GAG <i>P</i> : AGC <i>P</i> 60		ACA): .:	ATT' : : ACT' 270
600 600 600	0 · · 0 0 · · 0	170 GCCG ::::	240 ;aaga :::: ;aaga
40 GAG : GGA		1 14AG: 1:::	2 3GA .::
	100 116C 116C	.662 .: : AG2	CAC
10 20 30 40 50 GTAGCCGGGGGAACGGC-CGGCGCGCTTGCCGGTGGGCGGAGGCGAGACT-CCACA : ::: ::: ::: ::: ::: ::: ::: ::: :::	70 80 110 GCCG-GTCG-CCCGCGAGTGC-ACCCGCCATGCACCTGCCGC-CCGCTGCCGCAG :: ::: ::: ::: ::: ::::::::::::::::::	130 140 150 160 170 180 TGCTGCTGCTGCCGCGCGCGCGCGTGGCCTCCCGGAAGCCGACAATGTGCCAA : :::::::::::::::::::::::::::::::::	200 240 250 250 240 250 GGTGGACAACACGGCCAGGAAGAATTTCGGCGGC :::::::::::::::::::::::::::::
₽ 3.6 T	.:: 16C	160 1707 1007 1006	230 CAC(:::
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	90 CCA::	.: \GG(;AA(;
))	0, 00 1: 00 0: 00	.GCGJ : . :CGGZ 180	.: .: .GGT(250
G : GGG(ACCCC :::: ACCCC	0 GCG :: GCC	0 ATG ::: ATG
H H	0 U	150 0606 0606 0606	220 3GGA' ::::
3CGCT:::	80 AGT(:: AGC(ρς:	;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;
G :: :GGAC 30	8 ∴ : 0 - 7	.: :: :: :: :: :: :: :: :: :: :: :: :: :	ACC
1	CCGCC 100	140 GCCG ::::	210 ;TTCA ::::
20 66C 66C	O D	G G 1	2 4GT :::
	0 11 11 11 11 11)5 ::: 00 11 00 01	CAZ
666 ::: 666 20	06 90 90 90	TGCT(:::: TGCT(160	GGAC:::: GGAC 230
20 AACGGC-CGGCGCGCTTG ::: ::: :: :: GCCGGCGCGGCTGGGAGCGGGTGGG	0 :: U	130 16C : :	200 GGT :::
10 -GG, ANG	C-T	GCTAC'::GCCGC':50	GCT
.AC.	60 GCAGTT-CTC-T : ::: GGACCTGGAGCTCCG 80	GCTAC :: .: CTGCCGC 150	.: .: .: .: .: .: .: .: .: .: .: .: .: .
::: ::: ::: :::	60 TT-1 GAG 80	CCI	190 GGTGCCGGGC ::::::: GGTGCCGGGG
AGC 	CAG :.:	120 GGGCT ::::: GGGCT	190 rgcc(::::
	(120 3666 :::	.:: (GG!
10 cGTAGCCGGGGG : ::: .: h ACGCGTCCGCACANG	-9 	120 c rcgggcrgcrac : :::: :: :: H rggggcrccrgccgc 140	190 200 210 220 230 240 250 250 240 250 cdgccgccgccgccgccgccgccgccgccgccgccgccgc
O H	O H	U H	O H

Fig. 23F

TTA)0 14G	50 3.4.4 3.4.4 3.4.4	30 1.6T 1.6C
320 GAT ::: GAT	390 3CTA(::.	460 CTGA ::::	530 CTTG' : ::
GA(CA(::	CAC	: : : : : : : : : : : : : : : : : : :
Ö Ö H H O	GAG(::: GAG(410	ACA:::AGA:480	GAG ::: GAG 550
::::::::::::::::::::::::::::::::::::::	\ \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	CA CA SAA) 2AG 2AG
310 GGCJ : :: GCCJ	380 TGA(::	450 GTA(::.	520 CTC : :
U	CA CA		GT •:
ATT .:: ATT	7	TTCT:::	GTGG : :: GCGG 540
: : : : : : : : : : : : : : : : : : :	AAC. : .GGC-		.:: 566 567
0 H 0	370 TGG	440 GTG(:::	510 CAG ::: CAG
300 CAGT	7.1.1.3 7.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	4 34G 34G 34G	C
: 11 10 10 10	Ŭ : ⊞		AT(::: AT(
GAA5 GAG5 320	AACT:::::::::::::::::::::::::::::::::::	::: ::: ATT(3GAA 3 : : 3GCA 530
0 24 :: 0 24 :	CC 2.:	430 ACCI ::::	500 TCAG ::.
290 GTA :::	360 AAC :: AAT	4.3 AA(.: GA(5. GT(
.:: ::: :AA	 	1 :: H	ACT ACT
GTCC:::	GAA1 :::: GAA7 380	GCC(. : ATC(450	AGA(:: CGA(520
.HG .HG .HG	. Ω . Ω . Ω	O. GT.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
270 310 320 320 300 310 320 320 320 320 320 320 320 320 320 32	340 380 340 390 390 390 390 380 390 390 390 390 ACAGCAACGACTTTGAATGCAACCAACT-CTTGGAACAGCATGAGGAGCAGCTAG : :::::::::::::::::::::::::::::::::::	410 420 430 440 450 460 CACTGAAGAAGGAGTGCCCTAACCTATTTGAGTGGTTCTGTACACACAC	480 490 500 510 520 530 AGGCACCTATGGCCAGATGCCAGGGTGGGTCTCAGAGGCCTTGT :::::::::::::::::::::::::::::::
.: :: GA(.: ::: GA(AA(:• AG(AT(: AC(
:: :: AAA	CAAC :::: CAGC 370	AAG: ::: AAG: 440	CCT::CCT
3AGAU 3AAAU 300	3	0 IGP :::: IGP	CAC
270 GAG(:::	340 ;ACA(: :	410 ACT(.::	480 GGC ::
2000	3 [GA :::	3AC 3CA	TCCA:::TCCA
GTC ::: 0	.:. 0 1	GCAC::::	CTTC::::::::::::::::::::::::::::::::::
260 AACACGGCG ::::::: AACACGGCT 290	.::: :::: :TGT		irc.
260 .cacG .:::	330 9999 9999	400 GGT :::	470 ATGCTG' .:::: GTGCTG
2 (3 () () () () () () () () () (CTC	
260 310 320 GGCAACACGGCGTGGGAGAAGAGTCTGTCCAAGTACGAATTCAGTGAGATTCGGCTCCTGGAGATTA ::::::::::::::::::::::::::::::	330 340 360 360 370 380 390 390 390 390 390 390 390 390 390 360 380 380 390 390 360 380 380 380 380 380 380 380 380 390	400 AGGCCTGGTGGCAGA :::::::::: AGGCCTGGTGGCTGC 420	470 AGCATGCTGTCTTCC :: .::: AGTGTGCTGCTCTCC 490 500
260 270 280 320 310 320 320 320 310 320 320 320 320 320 320 320 320 320 32		400 c AGGCCTGGTGGCAGA ::::::::::: H AGGCCTGGTGGCTGC 420	
C H	S H	O H	O H

Fig. 23G

COFFOIR CHIES

Fig. 23H

830 840 860 870 880 GTGAAAATGTCAACGCTCCTACACATGTGAAGAGTGTGATTCTACCTGTGTGGG :::::::::::::::::::::::::::::	890 900 910 920 930 940 950 CTGCACAGAAAAGAAATGTAATCTCTGGCTACAGCAAGCA	960 970 1020 C GCAGATATAGATGCTCATTAGAAACAAAGGTGTGTAAGAAGGAAAATGAGAACTGCTACAATACTC ::::::::::::::::::::::::::::	1030 1040 1050 1060 1070 1080 1090 c cagggaggaggaggaggaggaggaggaggaggaggaggag
840 AACGGCTCCTACACATG:::::::::::::::::::::::	910 GTAAAGAGTGTATCTCT(::::::::::::::::::::::::::::::::	980 AACAAAGGTGTGTAAGAA	1050 GGAAGGTTTCGAGGAAGAC :: ::::::::::::::::::::::::::::::::::
830 TACTGTGAAAATGTCA :.:::::::::::::::::::::::::::::::::::	900 AAGGCCCAGCCAATTG ::::::::::::::::::::::::::::::::::	970 :GAATGCTCATTAGAA ::::::::::::::::::::::::::::::::	1040 GTCTGCGTGTGTCCGG ::::::::::::::::::::::
820 C GCAATGTACAGTACT :::::::::: H GCGCTGCGCAGTTCT 840 850	890 C CTGCACAGGAAAAGG :::::::::::: H CTGCACAGGGGAAGG 910	960 C GCAGATATAGATGAA :::::::::::: H GCAGATGTGGACGAG 980	1030 C CAGGGAGCTTTGTCT ::::::::::::::::::::::::::::::

Fig. 231

1110 1120 1130 1140 1150 AGGAAAGT——CCC—ACACACCCCTCCCATGAGGATTTGTGACGGGCATCCAG :.:.:.::::::::::::::::::::::::::::::	30 1240 1250 1260 1270 1280 1290 ATCAACCCCATTTCTCCAGGAAGTTTTGG-AGGAAGCTGCCTTTGAAACAGTAGATACTCACTT . : . : . : . : . : . : . : . : . : . :	
40 :: :3A 10 AGAAAATG: ::::::	1280 :TGAAACAGTZ :TCTAACGGTZ 1290 1350 ATTTTGATAC	 CCGCTAGA(
1100 1110 1140 AAGGCGAAGTGGCAGGGAAGT——CCC—ACACAGCCCTCCCATGAGGAT ::::::::::::::::::::::::::::::	0 ::::::::::::::::::::::::::::::::::::	370 1380 1390 ATAAAATTGATCATTGAAGGTCACCAGGAA
1130 :: .::::: GCTGCCCTCC 1160 1200 TGAGAGGACA' CAGAAGGATG'	1270 ::::::::::::::::::::::::::::::::::::	 AAAAAAAAA 1410
1120 CC-ACACACACACACACACACACACACACACACACACAC	1260 :: .:::: :: .:::: :: .:::: 0	:: :: aaaaaaaaa 0
.aAAGTC .: : .GAGAAAGC 1140 1180 .CACCCTTT .::::::	1250 GGAAGTTT GGAAGTTT 1260 1320 ATTTCTTG ATTTCTTG 133(1390 GAAGGTCACCAGGAA :.:::: ::::: GTAGGTAATCAAAAAAA 90
0 1110 GTGGCAGAGGA. : .::::: GCCACAGAAGG. 1130 1 1170 1 GCTGGACTCTC. : :::: GCCGGACTT1	1240 : :: :: :CTGCP 1310 AAAACGCTGC : : :::: AACA-GCTGC	1380 ATCATTGAA : :::::: ACCATTGTA
1100 ::: .::: AGGCTGAAGTGGCAG 1120 1120 1170 GTTCAGAAGCTGGAC: :::TAATGTGCCGGAC 1180	230 1240 ATCAACCCCATTTCT .:.:::::::::::::::::::::::::::::::	370 1380 ATAAATTGATCATT :::::::::::::::::::::::::::::::::
C AAG :: H AG 11160 C GT	1230 C ATC; : : H TGC; 1240 1300 C GGC; : :	1370 C ATA ::: H ATA

Fig. 23.

Covera to the state of the stat

3CTG 79	CCT 158	Q 16 CAG 220	R 36 CGC 280	P 56 CCT 340	CGG 400	V 96 GTG 460	s 116 TCG 520	R 136 CGC 580
rgca	CCAG	A GCC (F TTT	I ATC	P CCG	G GGA	A GCG	Y TAT
CAGC	AACC	L CTG (A GCT	TACC	STCT	R CGG	P CCA	I ATC
CTCTCCTCACGCTCGCGCAGTCTCCGCCGCAGTCTCAGCTGCAGCTG	CGGAGGAGGCGACAACTTCGCAGTGCCGCGACCCAACCCCAGCCCT	V GTC (R CGC	L	9 9	A GCG	Y TAC	G GGT
CGCA	zece7	L CIG (D GAC	A GCC	$_{ m CTG}$	V GTG	A GCG	s TCA
CGC	3TGC(A GCC (E. GAG	9 9	V GTG	$_{ m CTG}$	P CCT	D GAC
3TCT(CGCA(A GCA (S TCA	9 9	A.	V GTG	$_{ m CTG}$	N AAC
CGCA(ACTT(L CTG (S AGC	CIC	R CGG	E GAG	A GCA	P CCC
CTCG	ACAA	L CTG (D GAC	V GTG	R CGC	A GCA	V GTG	R CGC
CACG(3GCG/	P CCC (G GGA	g GGC	S AGC	E GAG	R CGC	$_{ m L}$
rccī	4GGA(L CTG (E GAA	Q CAG	P CCG	R CGG	F TTC	E GAG
CCTC		F FTC (L CTG	L CTG	P CCG	9 9	R CGG	s AGC
CAG	ACCC	L CTG 1	V GTT	P CCA	P CCA	R CGG	Y TAC	$_{ m L}$
2005	3GAG	O CAG (D GAT	A GCG	R CGG	S TCC	A GCC	A GCG
CTGCC	GGAC	A GCC (A GCA	D GAC	L	$_{ m CTG}$	E GAG	$_{ m L}$
CGTC	CACC	M ATG (L TTA	9 9	$^{ m Y}$	$_{ m T}$	N AAC	S TCC
GTCGACCCACGCGTCCTGCGGCCCCAGC	CAGGACTGAGCCGTGCACCCGGAGGAGACCCC		A GCT	A GCG	H	TACT	V GTG	V GTC
ZACGO	BAGCC	GGGTAGCCTGCAGC	A GCA	I ATC	V GTC	WTGG	K AAG	D GAC
BACCC	BACTO	PAGCC	P CCT	R CGC	H CAC	K AAG	V GTC	T ACC
ÓLC	CAGG	GGG1	A GCT	V GTG	C	V GTC	R CGC	L

90	90	90	90	252/:	361	90	90
15	17	19	21	23	25	27	29
64	70	76		88	94	100	106
	Q CAG	Y TAC	P	N AAC	N AAT	$^{ m Y}$	G GGT
K	A	A	Y	R	L	A	D
AAA	GCC	GCC	TAT	CGG	CTA	GCG	GAT
V	G	A	R	V	D	R	W
GTC	GGG	GCC	AGG	GTC	GAC	CGG	
K	S	Y	V		E	A	A
AAG	TCT	TAT	GTG	GGG	GAA	GCA	GCC
V GTC	${ m F}$	L	T ACC	CCC	A GCT	E GAA	A GCA
E	S	Q	Q	F	Y	E	Y
GAG	TCC	CAG	CAG		TAT	GAG	TAT
V GTG	F	E GAG	D GAT	ტ ელ	C TGT	$_{ m TTG}$	L CTG
A	A	P	s	D	YTAC	T	Q
GCT	GCT	CCG	TCG	GAT		ACA	CAA
D	Y	T	$_{ m L}$	M	V	L	g
GAC	TAT	ACC		ATG	GTG	CIG	GGC
S	R	A	W	D	D	K	T
AGC	CGC	GCC	TGG	GAC	GAT	AAG	ACG
S AGC	A GCC	I ATC	9 9 9	G GGA	Y TAT	E GAG	T ACC
D	S	H	A	Y	CIC	P	A
GAC	TCT	CAC	GCT	TAC		CCA	GCC
D	9	A	D	C	D	P	I
GAT	9	GCC	GAT	TGT	GAC	CCT	ATT
I	E	G	C	A	D	D	E
ATC	GAG	GGA	TGT	GCC	GAT	GAC	GAG
9	R	I	Q	E	P	GGT	A
9	CGA	ATT	CAA	GAG	CCG		GCA
H	$^{ m Y}$	R	E	R	D	L	G
CAC		CGC	GAG	CGA	GAC	CIG	GGT
Q CAG	CIC	A GCC	Y TAT	P CCA	V GTG	F	R CGG
V	F	c		T	V	L	E
GTC	TTT	TGT	990	ACC	GTG		GAG
E	V	A		Q	G	E	Q
GAG	GTC	GCC	GGG	CAG	GGT	GAA	CAG
C TGT	V GTC	E GAG	L	I ATC	Y TAT	GGA	C TGC

Fig. 24B

253/361 336 1180 416 356 1240 376 1300 396 1360 436 1480 456 1540 CCC S TCG G GGA A GCC GGT T ACA E GAA FTTC D GAC E GAA D GAT E GAA GGA E GAA Q CAG PCCC L R CGA G GGA E GAG S TCT FTTT D. GAC $_{
m ITG}$ $^{\mathrm{F}}$ $^{\mathrm{F}}$ A GCC PCCT E GAA L L CTG R CGC $C \\ TGC$ P CCA E GAG L CTA A GCA VGTG TACT Y TAC Q CAG M ATG LCTC K AAG N AAC K AAG $_{\rm CTG}$ I ATC V GTC S TCC TACG GGT S AGT 9 GGC V GTC N AAC A GCC E GAA P R AGG E GAA GGT E GAG I ATC E GAG D GAT $^{\mathrm{F}}$ P CCA PCCT S TCC E GAA $_{\rm CTG}$ A GCC A GCT PCCT R CGC N AAC L CTA $\frac{1}{1}$ TACC Y TAC E GAG S TCA S AGC S TCC E GAG I ATC M999 H CAC A GCC A GCA F TTC A GCC E GAG T ACA G GGG GGG G GGG K AAG P CCA VGTG G GGG TACG P CCA GGT D GAC N AAT PCCT I ATC TACA CCC $^{\rm C}_{
m TGT}$ PCCC E GAA S AGC R CGT C TGC R A GCC V GTC FTTC S TCC P CCA PCCG I ATC H CAC Q CAG E GAA V GTA 9 S TCT TACT M ATG S AGC TACT PCCT A GCT S AGT S TCC Q CAG E GAG L CTG ^Б Q CAG E GAG S AGC S TCC N AAC A GCC L T ACA GGA Q CAA 980 T ACA

Fig. 24C

				254/3	61		
476	496	516	536	556	576	596	616
1600	1660	1720	1780	1840	1900	1960	2020
D GAT	P	Q CAG	H CAT	PCCT	999 888	P CCA	G GGA
E GAG	L	$_{ m L}$	V GTC	S TCA	$_{ m ICT}$	L	s TCT
V	S	V	R	P	L	L	N
GTG	TCT	GTC	AGG	CCA	CTA	CTG	AAT
E	A	A	P	S	E	S	D
GAG	GCC	GCA	CCA	TCC	GAG	TCC	GAT
E	E	R	P	A	P	P	E
GAG	GAG	AGG	CCT	GCA	CCT	CCT	GAA
E	P	A	R	L	GGT	A	s
GAG	CCT	GCA	AGG	CIA		GCC	TCT
E GAA	9 9 9 9	P CCA	S	N AAC	G GGT	GGT	CCC
E	P	A	A	R	T	E	A
GAA	CCG	GCG	GCT	AGG	ACT	GAG	GCC
E	S	Q	E	E	A	S	E
GAA	AGC	CAG	GAA	GAG	GCA		GAG
E	S	S	S	R	E	S	$_{ m CTG}$
GAG	AGC	TCC	TCA	AGG	GAG	AGC	
E GAG	L	L	E GAG	P	GGG	G GGA	E GAG
K	E	S	G	TACT	V	T	R
AAA	GAG	TCA	GGA		GTG	ACA	AGG
E	S	K	D	P	E	E	T
GAG	AGC	AAG	GAT		GAG	GAG	ACC
E	P	E	P	L	R	E	GGT
GAA	CCC	GAG	CCT	CTG	AGA	GAG	
E	W	Q	L	T	A	S	E
GAA	TGG	CAG		ACT	GCA	AGC	GAG
D	A	A	P	E	E	EGAG	P
GAT	GCA	GCC	CCA	GAG	GAG		CCT
E	W	A	S	TACT	V	G	A
GAA	TGG	GCA	TCA		GTT	GGA	GCC
Y	L	P	A	P	L	R	R
TAT	CTG	CCA	GCA	CCT	CTG	CGA	CGG
K	A	E	GGT	P	T	P	T
AAA	GCT	GAG		CCA	ACT	CCT	ACA
E GAG	E GAG	TACT	PCCT	G GGA	S TCC	V GIC	A GCC

Fig. 24D

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636 2080	656 2140	672 2188	2267	2346	2425	2504	2583	2662	2730
A GCC	A GCC		IGGG	rgac	CCT	CGCC	SGAG	IGGA	
S AGC	T ACT		CCTA	CCAC	rcago	rgīgī	rccac	SCCTI	
D GAC	S TCA		rctac	SCCG	ATCC	GCCI	3GAG1	ACAAC	<i>r</i> \
TACT	9 990		ACCI	SAGCO	3AGC?	ATC	CICC	SAAAI	30080
PCCC	Q CAA	* TGA	racco	ATCC	CACAC	CTT	AACC	ATG	36060
$_{ m CTG}$	A GCC	T ACC	CTCT	rgrg2))))	ACTC	CCT	3TTT(AAAGO
V GTG	S TCT	V GTC	CATTO	ACCCI	SCCAC	SACTA	rcaco	SACTO	AAAA
P CCA	N AAT	T G G	CTT	CTTT?	rcrc	rttc	CTTC	TTT	AAAA
Q CAG	GGT	L	TTG	SCGT	CACAT	TAT	STCC	PATTI	AAAA
A GCC	S TCA	Q CAG	STCCI	TCC	GCT	GGCC	GGAC	SAAGT	AAAA?
Q CAG	A GCA	L CIG	CCT	AGCTO	CTGTO	GCT	SCCTO	CTGTO	AAAA
S V Q A Q P V L P T D S A TCA GTG CAG GCC CAG CCA GTG CTG CCC ACT GAC AGC GCC	V P A S G N S A Q G S T GTC CCC GCA TCA GGT AAT TCT GCC CAA GGC TCA ACT	F P L Q L W V T * TTC CCC CTG CAG CTC TGG GTC ACC TGA	ACTCI	rctc2	CACC	rcago	3GAA(ACTTO	AAAA
S TCA	V GTC	F TTC	CCAA	3GTA!	CCCT	BCCT	rcag(AACT2	ACCA
T ACC	V GTG	F TTC	CATCO	rgTG	1666	rgcad	SATCI	AAGC7	rgta?
G GGG	A GCC	L	CCAT	ACCTI	CCAT	CTAT	ratt(CCTT	SCTT
A GCA	· V GTG	L	CCAC	ATCCA	CTG	rcacc	CTCCI	AGAGO	AACCC
P CCA	G GGA	L CTA	rtaac	GAT	CTTC	TCAI	TGC	CCACA	ATTA.
T A P A G T ACT GCC CCA GCA GGG ACC	S R G G V GC CGA GGT GGA GTG	L S I L L L TC TCT ATC CTA CTC CTT	CTGTAGTCCTTTAACCCACCATCATCCCAAACTCTTCCTGTCCTTTGCCTTCATTCTTTACCCACCTCTACCTATGGG	CTCCAATCTCGGATATCCACCTTGTGGGTATCTCAGCTCTCCGCGTCTTTACCCTGTGATCCCAGCCCCGCCACTGAC	ATCTGTGACCCTTCCCTGCCATTGGGCCCTCCACCTGTGGCTCACATCTCGCCAGCCCCCACAGAGCATCCTCAGGCCT	TCCAAGGGTCCTCATCACCTATTGCAGCCTTCAGGGCTCGGCCTATTTTCCACTACTCCCTTCATCCGCCTGTGTGCCC	TCCCCTTTAGCTGCCTCCTATTGATCTCAGGGAAGCCTGGGAGTCCCTTCTCACCCCTCAACCTCGGGAGTCCAGGAG	ACCCGTACCCCCACAGAGCCTTAAGCAACTACTTCTGTGAAGTATTTTTTGACTGTTTCATGGAAAACAAGCCTTGGA	ATAAATCTCTATTAAACCGCTTTGTAACCAAAAAAAAAA
TACT	R CGA	S TCT	TAG	CAA1	TGTC	ZAAGC	CCT	CGT	AAATC
R GA	ე ე	I I I	CTC	CT(AT(ŢĊĆ	ĪĊ	ACC	ΑTZ

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Fig. 24F

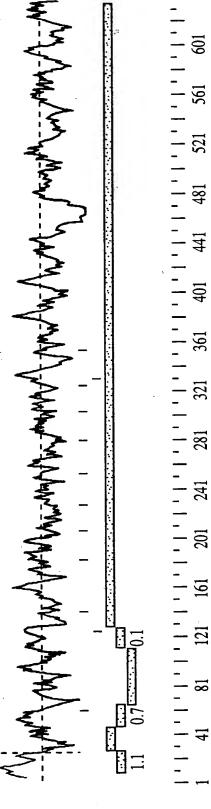


FIG. 24F

Cys Negly out ins

<u>ooysolen ettent</u>

70 RPPPSRRA ::::::: RPPPSRRA 70	140 GIYRCEVQ ::::::: GIYRCEVQ 140	210 CDAGWLSD :.	280 ARAYCQER ::::::: ARAYCQER 220	350 NKHSRFNV ::::::: NKHSRFNV 290
60 LTIPCHVHYL ::::::::: LTIPCHVHYL 60	130 ALSELRPNDS :::::::: ALSELRPNDS	200 YAAYLGGYEQ	270 DPPEKLTLEE :::::::: DPPEKLTLEE 210	340 FLFPNQTGFP ::::::::: FLFPNQTGFP 280
50 APLQGVLGGA ::::::::: APLQGVLGGA 50	120 (PASLTDVSL.::::::::::::::::::::::::::::::::::::	180 190 200 210 SGAQEACARIGAHIATPEQLYAAYLGGYEQCDAGWLSD :.	260 EDLNGELFLG: ::::::::::::::::::::::::::::::::::	330 SGGLPGVKTL SGGLPGVKTL 270
40 AFRVRIAGD? ::::::::: AFRVRIAGD?	110 .YRFRVALPA) ::::::::::::::::::::::::::::::::::::	180 GAQEACARIC 	250 DLYDVYCYAE ::::::::::::::::::::::::::::::::::::	320 PIVTPSQRCC ::::::::: PIVTPSQRCC 260
20	90 100 110 120 120 140 GREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ ::::::::::::::::::::::::::::::::::::	160 KGVVFLYREGSARYAFSFS	230 240 250 260 270 280 280 270 280 XGDMDGFPGVRNYGVVDPDDLYDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQER::::::::::::::::::::::::::::::::::::	300 340 350 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 350 350 350 350 350 350 350 350 35
20 LAQAPAALAD ::::::::: LAQAPAALAD 20	90 RGREAEVLVA :::::::: RGREAEVLVA 90	160 VKGVVFLYRE 		300 WDGGLDHCSP:::::: WDGGLDHCSP
10 MAQLFLPLLAALVL ::::::::::::: MAQLFLPLLAALVL 10	80 VLGSPRVKWTFLSR ::::::::::::::::: VLGSPRVKWTFLSR 80	150 HGIDDSSDAVEVKV :::::::: HGIDDSSDAVE	220 QTVRYPIQTPREAC : :::::::: QRYPIQTPREAC 160	290 GAEIATTGQLYAAW ::::::::::: GAEIATTGQLYAAW 230
332 BEF	332 BEF	332 BEF	332 BEF	332 BEF

Fig. 24G

ა ა ა ა	х ч ч	1 : 1 1 : 1	O O	
ტ ტ	440 450 460 470 480 ETQSMVPPTGFSEEEGKALEEEEKYEDEEEKEEEEEEEVEDEALWAWPSELSSP:::::::::::::::::::::::::::::::::		560 570 580 590 600 610 620 332 VEAREVGEATGGPELSGVPRGESEETGSSEGAPSLLPATRAPEGTRELEAPSEDNSGRTAPAGTSVQAQP :::::::::::::::::::::::::::::::::::	
IMEDGGG ::::::: IMEDGGG	VAWP S:::	VLASPS	PAGT	
.410 (SIPI) (SIPI) 350	480 EALW: :::: EALW: 420	550 PRERN :::: PRERN	620 RTAP:	
GAIYS: ::::: GAIYS	13A3	LPTE : LPTE	DNSC	
400 ESESR ::::: ESESR 340	470 EEEEE ::::: EEEEE	540 PPTET ::::: PPTET	610 EAPSE	
4 : : ATE	XEEE 4 XEEE 4	5 VHGP :::: VHGP	9 3ELE3 38	
OLPQI :::) EEE1	(PPR)	EGTRE :.: GAR-	F
390 :::: 330	460 KYEI ::::	530 EASF ::::	600 TRAE	670 670
370 380 390 400 410 ASNPASNPASDGLEAIVTVTETLEELQLPQEATESESRGAIYSIPII::::::::::::::::::::::::::::::	440 450 460 470 480 ETQSMVPPTGFSEEEGKALEEEEKYEDEEEKEEEEEEEVEDEALWAWPSEL ::::::::::::::::::::::::::::::::::::	0 520 530 540 550 GPEASLPTEPAAQEKSLSQAPARAVLQPGASPLPDGESEASRPPRVHGPPTETLPTPRERN :::::::::::::::::::::::::::::::::::	LLPA	650 660 670 PASGNSAQGSTALSILLLFFPLQLWVT :::
0 IVTV :::: IVTV 0	O GKAL :::: GKAL O	0 SPLP SPLP SPLP O	0 GAPS	O LLLF
380 GLEAI ::::: GLEAI 320	450 SEEEG ::::: SEEEG 390	520 QPGAS ::::: QPGAS 460	590 688EG	660 ALSIL
PASD0:	PTGE	AAVL(:::: AAVL(SEET	ZGSTZ
370 SNPASNI : TQPPTQI 310	440 SMVPI ::::3 SMVPI 380	510 QAPAI ::::: QAPAI 450	580 PRGES ::: PRG	650 GNSAÇ
3. ASNP.		SLSC	0 570 580 VEAREVGEATGGPELSGVPRGE ::::::::::::::::::::::::::::::::::::	
O SAIPE 	3	AQEK ::: AQEE	0 GGPEL ::::: GGPEL 0	VAVV
360 YCFRDSAQP-SAIPE. :::::::: YCFRDSAQLLPSLRP 300	430 APRT:::	500 TEPA :::: TEPA 440	570 EATG: :::: EATG	640 SRGG
YCFRDSAQ ::::::: YCFRDSAQ 30	DPAE; :::: DPAE;	ASLP'	KEVG]	rdsa.
YCFF ; YCFF	20 TPEI :::: TPEI 60	90 GPE7 :::: GPE7	60 VEAR :::: VEAR 00	630 640 332 VLPTDSASRGGVAVV BEF
332 BEF	420 332 T : BEF T 360	490 332 G : BEF G 430	560 332 V. : BEF V. 500	630 332 V BEF -

Fig. 24F

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		,		
RPRSRRA	SVYRCEVQ	CDAGWLSD	ARDYCLER :.:::: ARAYCQER 280	KQNRFNV ::::: IKHSRFNV 350
60 IPCHVHHLI::::::::::::::::::::::::::::::::::	130 SELRPNDSC::::::	200 AYLGGYEQC :::::::: AYLGGYEQC 200	270 PSKLTWEE <i>R</i> : ::::: PEKLTLEE <i>R</i> 270	340 FPNQTGFPS ::::::: FPNQTGFPN
50 KGVLGGALA ::::::: QGVLGGALT 50	120 SLTDVSLVL :::::::: SLTDVSLAL 120	190 [ATPEQLYA ::::::: [ATPEQLYA 190	260 NGELFLGAP: ::::::::	330 :PGVKTLFL::::::: :PGVKTLFL:
40 'RI-GAAQLI :::::: 'RIAGDAPL(110 (VALPAYPAS ::::::: (VALPAYPAS 110	180 ACARIGAR::::::::::::::::::::::::::::::::::	250 VYCYAEDLN :::::::: VYCYAEDLN 250	320 PSQRCGGGI ::::::::
20	90 100 110 120 130 REVEVLVARGLRVKVNEAYRFRVALPAYPASLTDVSLVLSELRPNDSGVYRCEVQ ::.::::::::::::::::::::::::::::::::::	150 160 170 180 200 IDDSSDAVEVKVKGVVFLYREGSARYAFSFAGAQEACARIGARIATPEQLYAAYLGGYEQCDAGWLSD ::::::::::::::::::::::::::::::::::::	230 240 250 260 270 GDMDGYPGVRNYGVVGPDDLYDVYCYAEDLNGELFLGAPPSKLTWEEARDYCLER ::::::::::::::::::::::::::::::::::::	30 340 GGLDRCSPGWLADGSVRYPIITPSQRCGGGLPGVKTLFLFPNQTGFPSKQNRFNV ::::::::::::::::::::::::::::::::::::
O ALADDLKED ::::::: ALADVLEGD	90 VLVARGLRV :::::::: VLVARGVRV 0	160 FLYREGSARY ::::::::: FLYREGSARY 60	230 DGYPGVRNYG :::::::: DGFPGVRNYG 30	300 DRCSPGWLAD :.:::::: DHCSPGWLAD
	1.SGDREVEV::::::::::::::::::::::::::::::::::	16(VKVKGVVFL) :::::::: VKVKGVVFL)		30 AAWNGGLDR :::::::: AAWDGGLDH 300
10 MIPLLLSLLAALVLT : .:.::::::: MAQLFLPLLAALVLA 10	70 80 M APGFPRVKWTFLSGD .:::::::: H VLGSPRVKWTFLSRG	0 HGIDDSSDAVEVKVK ::::::::::::: HGIDDSSDAVEVKVK 150	10 220 QTVRYPIQNPREACS :::::::::: QTVRYPIQTPREACY 220	280 290 M GAQIASTGQLYAAWN:::::::::::::::::::::::::::::::::::
M MIE : : H MAC	70 M APC . : H VLC	140 M HG] ::: H HG]	210 M QTV ::: H QTV	280 M GAÇ :::

Fig. 24I

<u>normalen netenl</u>

SECONDIANTESASSE SECONDIA S
0 390 400 410 EKLEELQLPQEAMESESRGAIYSIPISEDGGGGG : ::::::::::::::::::::::::::::::
0 390 400 410 EKLEELQLPQEAMESESRGAIYSIPISEDGG ::::::::::::::::::::::::::::::::::
0 390 400 EKLEELQLPQEAMESESRGAIYSIPISEI ::::::::::::::::::::::::::::::::::
EKLEELQLPQEAMESESRGAIYSIPI : : : : : : : : : : : : : : : : : : :
0 390 400 EKLEELQLPQEAMESESRGAIYS] : : : : : : : : : : : : : : : : : : :
0 390 400 EKLEELQLPQEAMESESRGAI 390 460 ETLEELQLPQEATESESRGAI 390 460 EEERFKDLEALEEEKEQED ::::::::::::::::::::::::::::::::::
0 390 4 EKLEELQLPQEAMESESRG 390 400 390 400 ETLEELQLPQEATESESRG 390 400 EEERFKDLEALEEEKEQET ::::::::::::::::::::::::::::::::::
0 390 EKLEELQLPQEAMESE : :::::::::::::::::::::::::::::::::::
0 390 EKLEELQLPQEAME 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0 390 EKLEELQLPQE 390 0 460 EEERFKDLEAL 460 10 10 10 10 570 GPSLLPATWAP 570 GPSLLPATRAP 640 640 640 610 110 120 131 140 640 640 610 610 610 610 610
0 3 EKLEELQLE 390 4 ETLEELQLE 390 4 EEERYEDLE :::::::: PDGESEASP 570 530 570 640 640 6C CLEEKEGFR
0 EKLEEL 390 390 EEERFK :::: PG PG PG S70 GPSLLP S70 GPSLLP APSLLP APSLLP APSLLP
0 E K L E C C L E C C C C C C C C C C C C C C
OH OH OH OH O A O A
3380 3380 3380 3380 3380 3380 3380 3380
XALE STED SOOT SOOT SOOT SOOT SOOT SOOT SOOT SOO
GLEAIN ::::::: 380 380 380 :::::: VLQLDP VLQLDP :::::: FAGSSS :::::: ETGSS- 630 630 PSPCHN
0 · 0 · 0 · 0 · 0 · 0 · 0 · 0 · 0 · 0 ·
370 D0 D0 D0 D0 D0 D0 D0 -
SSPAS SNPASNPA 370 370 370 10SIAPPT 10SMVPPT 440 50 50 50 510 50 520 520 440 520 520 520 440 530 530 530 530 530 530 530 530 530 53
PAS:
8 : S
370 SEASSPAS :::::::::::::::::::::::::::::::::
360 CFRDSAHPSASSE ::::::::::::::::::::::::::::::::::
360 360 360 360 360 500 666 666 67 666 67 67 67 67 67 67 67 67
36 CFRDSAHPS ::::::::::::::::::::::::::::::::::::
FRDS FRDS FRDS 420 DPAH 1::: ASLH ASLH EARH EARH 1::: 1::: 1::: 1::: ASLH 1::: ASLH 1::: 1::: ASLH 1::: 1::: ASLH 1::: 1::: ASLH 1::: 1::: ASLH 1::: 1::: ASLH 1::: 1::: 1::: ASLH 1::: 1::: 1::: 1::: 1::: 1::: 1: 1
PA·PA G. G. G. G. G. G. G. G. G. G. G. G. G.

Fig. 24J

740	WSDGAPLLY::.	LLF	810 SRPRLRYAV		880 (APLTPPSS
730	IDRTIEGDFLV		800 PQLPLAQIFO	ŌTd	870 PRGQLSRHRI
720	YREYQWIGLN:	099 -T	790 KMGLVSCGPE		860 ALRSMDAPEG
710	PEEQDFVNDR		780 PCNYHLSYTC		850 ISCVPRRPGR
700	AESQCRALGAHLTSICTPEEQDFVNDRYREYQWIGLNDRTIEGDFLWSDGAPLLY ::	IS	760 770 780 790 800 810 810 ENCVVMVWHDQGQWSDVPCNYHLSYTCKMGLVSCGPPPQLPLAQIFGRPRLRYAV		830 840 850 860 870 880 NLPLIRCOENGLWEAPQISCVPRRPGRALRSMDAPEGPRGQLSRHRKAPLTPPSS :: 670
069	WEEAESQCRA		760 LSGENCVVMV	· 任	830 AQRNLPLIRC
680	M GACYKHFSTRRSWEE		750 M ENWNPGQPDSYFLSG	· 山 	820 DTVLRYRCRDGLAQRI
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Fig. 24k

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) CAGT ::::	120 AGGCGA :::: GCAA	90 TGCC: :: : TGTC	260 GCTCA(::::. GCTCG(240	330 CCTCA ::: . CCTGG
50 60 60 60 60 60	12 GGA(15 TCCJ : ::	26 CAG(::::	333
CTC:	GGA	TGT:	;AGA; ::: AGA;	.: .: .: 300
CACG	110 .cccc .: : :	180 CCAGC' : .: ACCAC'	250 GAAGG .:::. AAAGA	320 TCGGC : ::: TGGGC
40 CCTC :::	1. GAC(::: GAC(16 GCCC	2. TGGZ ::.	32 GCT(GCT(
20 30 40 50 CGTCCGTCCTGCGCCCCCAGCCTCTCCTCACGCTCGCGCAGTC ::::::::::::::::::::::::::::::::::::	0 100 110 G-CTGCAGCTGCAGCCGTGCACCCGGAGGAGCCCCC : :::::::::::::::::::::::::::::::	40 150 160 170 180 190 CGCGACCCAACCCCAGCCTGGGTAGCCTGCAGCATGGCCCAGCTGTTCCTGCCC ::::::::::::::::::::::::::	10 220 230 240 250 260 GTCCTGGCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAG ::::::::::::::::::::::::::::::::::::	300 310 320 330 CGCGCCACTGCAGGGCGTGCTCGGCGGCGCCCT ::::: :::::::::::::::::::::::::::::::
0 AGC(.::	100 CCGG2 ::::	170 GCAGC::: GCAGAN	240 AGATG' .::: TGATG' 220	310 CAGG(::::
30 30 30 30 30 30	1 (ACC .:	1 CTG: 	2 GCA ::.	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
CGGC::: CGCG	STGCA(: : . SCGTG(ragc :. rg	rtra : :CCTC	CCAC
20 CCTG: CCCG	90 GCC: .:	160 CTGGGTAG .::. AGTG-	10 220 230 GTCCTGGCCCAGGCTCCTGCAGCT7::::::::::::::::::::::::::::::::::::	300 CGCG ::: CGCG
2 -GTC :::	ACTGA:::.:	CCCI	2 2160 3160	3 3 3 3 3 3
 CTG(30	.::: .:: 	CAG(CTCC	80 290 GCGTGCGCATCGCGGGC :::::::::::::::::::::::::::::::
TOL	80 1GCA 1GCG	150 AACCC ::: ATC	220 CAGGC :::: CAAGC	290 TCGC ::: TCG-
-144 -::	AGC1 .::: GGC7	150 CCAACC :::: -CATC- 140	3000 3000	3CA1
-cGTCC :: :: :GCGCCC		GAC	CTG:::0	.:: .::: .:::
GCTG	70 AG-C .::	140 CCGC	210 GGTCC ::::: GGTCC 190	280 CGCGT ::::: CGCGT
10 -CG :: GCGA(0 CGCAGTCTCA :::::::: CGCAGTCTCG 80	GTG	CCTG CCTG	TITC
1 CCA- CCGG	CAGT:::	GGCA	0 GCAGC ::::: GCCGC	0 GCGCT : :: GAGCC 250
-ACCCA .::: CTCCCG)5225 ::::: 9225	130 CTTC CTTC	200 GCTGGC :::::: GCTGGC	270 CCGC :: TCG2
10 GTCG-ACCCA-CG :. : .:: :: GAGGCTCCCGGCGAG	60 70 80 90 100 110 120 TCCGCCGCAGTCTCAG-CTGCAGGACTGAGCCGTGCACCCGGAGGAGCCGCGAGGGGGGGAGCGGAGGCGGA : ::::::::::::::::::::::::::::::::::	A.A T.T	200 210 220 230 240 250 260 CTGCTGCTGCTGCTGCTTTTAGCAGATGTTCTGGAAGGAGACAGCTCAGCTCAGCTCTGGCAGCTCTCAGCTCTTTTTTTT	270 280 300 310 330 AGGACCGCGCTTTTCGCGTGCGCTTCGCGGGGCGTGCTCGGCGCGCCCTCAC ::::::::::::::::::::::::::::::::
H Z	H M	H CA. M -G'	υ Ο	H N

Fig. 24I

OOFEDIAC CLIECT

340 350 360 370 380 400 CATCCCTTGCCACGTCCACTGCGGCCACCGCCGGGCTGTGCTGGGCTCTCGCGGGTC ::::::::::	410 420 430 440 450 460 470 AAGTGGACTTTCCTGTCCCGGGGCCGGGGGGGGGGGGG	ACGAGGCCTACCGCGTGCCTGCCTACCCAGCGTCCCCCGACGTCTCCCTGGCGCT ::::::::::::::::::::::::	620 630 640 650 660 670 680 GACGCTGTGGAGGTCAAAGGGGTCGTCTTTCTCTACCGAGAGGGCTCTGCCCGCTATGCTTTCT :::::::::::::::::::::::::::::::
310	4 H AAGTG ::::: M AAGTG 380	4 ACGAG ::::: M ACGAA 450 50 H GAGCG ::::: M GAGCG	6 H GACGC :: :: M GATGC 590

Fig. 24M

OOPEOLEO CLIEDI

.:: .::	ATC:::	 	0 : 0 0 : 0	ACG
750 CTA1 ::::	820 CCC7 CCC7	90 GGJ GGJ	960 TGAC : :	30 CC7 30
7 ;;c ;;;	8 NTC 	8 161 151	e :: .: .:	1030 CCACC
CAGC:::: CAGC	GT2 ::: GT2 90	3GT 3GT 3GA	.crgc ::.: crac	16C 36C
.: 125 125 125 125 125 125 125 125 125 125	:: :: 75	'AT(: 'AC(ည်	ATTG::::;ATCG:
740 CGGA ::::	810 CGTG :::	880 AACT ::::	950 TGTT :::: TGTT	20 3AG ::
2000	00 00 00 00 00 00 00 00 00 00 00 00 00	86 687 ::: 687	9 0 1 1 1 1 1 1 1	1020 CAGA(:: :
CACC::::	CAGA :::: CAAA 780	500 500 500	AGAA :::: AGAA 920	6616 :::: 6616
00 720 730 740 750 :AGGAGCCTGTGCCCCATTGGAGCCCCACCCCGGAGCAGCTCTATGC ::::::::::::::::::::::::::::::::::::	10	40 850 860 870 880 890 890 890 890 890 890 890 890 890 890 890 890 890 890 820 830 840 850 860 860	10 920 930 940 950 960 ATGATGTGTACTGAAGACCTAAATGGAGAACTGTTCCTGGGTGACCC ::::::::::::::::::::::::::::::::::	80
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0)0 3GA ::	0 3 3 3 5 5 5 5 7	10 11G 11G	0. 3. 5. 5. 5. 5. 5. 6.
730 CATC ::: AATC	8008 	870 CCGG : :: CTGG	940 AAAT(:::: AAAT(1010 GAGC(:::: GAAC(
CA ::06.		ΣΕΙ ΣΕΙ		. : . : G . T G
3007 3007 3007	3GCT(:::: 3GCT(CTT:::0.24	3ACC; :::: 3ACC; 910	GCCA(: :: GTCT(980
:: ::		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 iaa(:: iaa(
720 ITGG I.::	790 TGGC:	860 3ATG ::::	930 CTGA.	1000 GTAC
CA::0	:: 0 :: 0	ы. Б.: Б.	ў ў О	
069 12521 12521	3ATG(:::: 3ATG(760	ACA :::		3666 3666 3666
0 :: 5	0 GT(GT(0 AG/ S::	0 H ·· H	O CAC
710 rgrgi	780 \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	850 366A :::	920 FACT ::::	990 AAGC
	0 6C7 0	TAC: TCJ	1 E C C C C C C C C C C C C C C C C C C	GG <i>F</i> :::3 GG <i>F</i>
1660 1: 1860 680	::: ::: :GAG	:: :: :: :: :: :: ::	ATGT(.::: ATGT(890	3GAG(::: 3GAG(960
0 GG7 GG7	0 TAT ::: TAT	0 0 0 0 0 0	0 TG7 TG7	0 1110 1110
700 CAG :::	77	840 GGC :::		
	7 TGGGGG :: :: CGGCGG	464 ::: 464 0	CTCT	1.02 1.02 1.02 1.03
: : .GAG 670	'TGG(:: 'CGG(740	.:: .:: .CGA(ACC': : : ATC'	970 AGAGAAGCTGAC . ::::::: AGCAAGCTGAC
0 : : : : : : : : : : : : : : : : : : :	760 CCTACCT ::::::	0 :: 0 0 :: 0 0 :: 0	00 GATGAC ::::: GATGAT 88	SAP SAP SAP
690 TTC:	760 TAC ::: TAC	830 CCC ::	900 GGA :: TGA	970 GAG
	760 CGCCTACCTTGGGGG ::::::::::: TGCCTACCTCGGCGG	830 840 850 860 870 870 890 CAGACCCCACGAGAGGCTTACGGAGACATGGATGGCTTCCCCGGGGTCCGGAACTATGGTGGTGG ::::::::::::::::::::::::::::	900 ACCCGGATGACCTCT . ::::::::::::::::::::::::::::::::::::	\ddot{c} \ddot{c}
9	7	ω	ထ	ത
Ξ	H Z	ΕΣ	H Z	H Z

Fig. 24N

1040 1050 1060 1070 1080 1090 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1100 1030 1040 1050 1060 1100 1170 1170 1150 1160 1170 1170 1170 1180 1140 1150 1160 1170 1170 1180	1180 1200 1210 1220 1230 1240 H CTTCCCCAACCAGCTTCCCCAATAAGCACAGCCGCTTCAACGTCTTCCGAGACTCGGCC ::::::::::::::::::::::::::::::::	1250 1260 1270 1280 1290 1300 1310 H CAGCCTTCTGCCATCCCTGAGGCCTCCAACCCAGCCTCTGATGGACTAGAGGCTATCG ::::::::::::::::::::::::::::::::::::	1320 1330 1340 1350 1360 1370 1380 H TCACAGTGACCAGGAGGAACTGCAGCTGCCTCAGGAAGCCACAGAGAGTGAATCCCGTGGGGC ::::::::::::::::::::::::::::
---	--	--	---

Fig. 240

00 1410 1420 1430 1440 1450 CATCATGGAGGAGGAGGTGGAAGCTCCACTCCAGAAGACCCAGCAGAGGCC ::::::::::::::::::	1460 1470 1480 1490 1510 1520 CCTAGGACGCTCCTAGAATTTGAAACACAATCCATGGTACCGCCCACGGGGTTCTCAGAAGGAAG	1530 1550 1560 1570 1580 1590 AGGCATTGGAGGAAGAATATGAAGATGAAGAAGAAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAG	1600 1620 1630 1640 1650 GGAGGATGAGGCTCTGTGGCCCCAGCGAGCTCAGCAGCCCTGAGGCCTCTCTCCCCACT ::::::::::::::::::::::::::::::::::::	1680 1690 1700 1710 1720 CCAGGAGAGATCACTCTCCCAGGCGCCAGCAAGGGCAGTCCTGCAGCCTGGTG .::::::::::::::::::::::::::::::::
1420 1430 GGAGGAGGTGGAAGCTCCA ::::::::::::::::::::::::::::::::::	70 1480 1490 1500 GAATTTGAAACACAATCCATGGTACCGCCCACGGGGTT ::::::::::::::::::::::::::::::::	1560 1570 AGATGAAGAAGAAAGAG(::: AGACTTGGAG(10 1620 1630 1640 GTGGGCATGGCCCAGCGAGCTCAGCAGCCCGGG :::::::::::::::::::::::::::	1700 CCCAGGCGCCAGC :::::: CCCAGGTGTCCCCACCAGC
	1470 1480 CTAGAATTTGAAACAC ::::::::::::::::::::::::::::::::	1540 1550 1560 GAAGAAGAATATGAAGATGAAGA :::::::::::::::	1610 1620 TCTGTGGGCATGGCCCA(::::::::	1670 1680 1690 GAGCCAGCCCAGGAGAAGTCACTCCCCAGG- :. :: :: :::::::::::::::::::::::::::::
1390 14 H CATCTACTCCATCCC ::::::::::::: M CATCTACTCCATCCC 1350 1360	1460 14 H CCTAGGACGCTCCTA ::::::::::: M CCCAGGACTCCGCTA 1420 1430	1530 15 H AGGCATTGGAGGAAG. : :::::::: M TAGCCCTGGAGGAAG. 1490 1500	1600 H GGAGGATGAGGCT' :::::: M GGAGGAC-(1670 H GAGCCAGCAGCC(:.:::: M GGCTCAGAAAC1600

Fig. 24P

1780 1790 GTCCATGGACCACCTACTGAGAC ::::::::::::::::::::::::::::::::::	1850 1860 CTGGTTGAGGCAAGAGGTG ::::::::::::	1930 ACAGGAAGCTCC- .:::::::::::::::::::::::::::::::::::	1990 2000 GGAGCTGGAGGCCCC ::::::::::::::::::::::::::::::	2060 2070 CCAGTGCTGCCCACT :::::::::::::::::::::::::::::::::
1770 1780 1790 GGCCTCCAAGGGTCCATGGACCACCTACTGAGAC ::::::::::::::::::::::::::::::::::::	40 1850 CTTCCACTCTGGTTGA ::::::::::::::::::::::::::::::::	1920 GAGAGAGCGAGGAG ::::::::::::::::::::::::	1980 TGAGGGTACCAGGG::::::::::::::::::::::::::	2050 20 GTGCAGGCCCAGCC :::::::::::::::::::::::::::
1750 1760 1770 1780 1790 ATGGAGACTCCAGGCCTCCAAGGGTCCATGGACCACCTACTGAGAC ::::::::::::::::::::::::::::::::::	1820 1840 1850 1860 GGAGAGGAACCTAGCATCCCCATCACCTTCCACTCTGGTTGAGGCAAGAGGGTG ::::::::::::::::::::::::::::::	1890 1900 1910 1920 1930 GGTCCTGAGCTATCTGGGGTCCCTCGAGGAGGAGGGAGGAGGAGGAGGAGCTCC- ::::::::::::::::::::::::::::::::::	1950 1960 1970 1980 1990 2000 CTTCCCTGCTTCCAGCCCACAGGGCCCCCTGAGGGTACCAGGGAGCTGGAGGCCCC ::::::::::::::::::::::::::::::	2020 2030 2040 2050 2060 2070 TGGAAGAACTGCCCAGCAGGACCTCAGTGCAGGCCCAGTGCTGCCACT ::::::::::::::::::::::::::::::::::
		1890 13 FGGTCCTGAGCTATCT .:::::::::::::::::::::::::::::::::::		2020 2030 CTGGAAGAACTGCCC :::::::::::::::::::::::::::::::::
1730 1740 H CATCACCACTTCCTG :::::: M CGTCACCTTCTCTG	1800 1810 H TCTGCCCACTCCCAG : ::: :::::: M TTTGCTCCCCCGAG	1870 1880 1890 1900 1910 1920 1930 H GGGGAGCAACTGGTCCTATCTGGGGTCCCTCGAGGAGAGCGAGGAGACAGGAAGCTCC- ::::::::::::::::::::::::::::::::::	1940 HGAGGGTGCCC ::::::: M GCTTGGAGGATGGCC 1840	2010 H CTCTGAAGATAATTC :::::::::::: M CTCAGAAGAGAAGTC 1910

Fig. 240

CTCA : . : : CACA	CCT	200 CTTT :::	-TTT :: ATCT	 AG
0 GC1 :: CC2	cct ::: gacct	2200 CCTT' :::	1 : :	 GAC
2130 AAGG. .: CTGC		TAGT(.:: AAGCZ	: : : : : : :	 1AT
2 ::: :::2040	 GGGG	2200 TAGTCCTTT .:: ::: ACAAGCACTTT 2180	2230 CTGTCC :::::: CTGACC 2250	70 CTC- ::: CTCA 2320
TGCCC .::: AGCCC 204	 ATG	CTP	2230 -CTGTCC- ::::: TCTGACCA 2250	2270 CTC ::: GGCTC 232
2130 CTGCCCAAGGCTCA :::::::::::: CCCAGCCCCTGCCACA 2040	D D	90 CCTG CCTG	CAT	
TCC	50 CCTA- :: CCAG(2190 CC :: AGCC	C : TGCT(240	3.6G. 3.0 3.0
 GTAT 2030	2150 CCTA-CT :::: TGCCAGGCTAT 2100	21; ;A(; ;GGAG(C : :GTGC' 2240	ATGG(.::: .GTGG; 2310
2120 AATT .::	2 TTT	180 2190 GTCACCTGACCTG- : : ::: GAGGCCTTCCAGGGAGCCTGC 2160 2170	T - L	2260 TCTACCTATGGGT- . ::::::: AGTACCAGTGGATT 0
2 3TA 3TG	4T- :: 4TG	-AC .:	CTCT	2260 CTAC: ::: GTAC
10 CATCAGGTAA :::::::: CATCAGGTGA 2020	CTAT :::: GCCTAT	0 GTC: .GGCC	2220 TCCCAAACTCT- : ::.::: TGCCGAGCGCTA	T(GGGA(2300
0 ATC ::: ATC	CT :: CTGC	2180 GT : :GGAGC	22 CCP ::: 22	
2110 CGCA' :::	0 CCTC	21 GGG	- TC : GTG	-ACC: ::: TACC
21 CCCG ::: FCCCT	2140 CCTCTCTAT- :::::::: TTTCCGCTGCCTATG 80 2090	1 H 1 U 0 U	TCA-1::::::::::::::::::::::::::::::::::::	C C C C C C
GGTC(::	21, GGTT	2170 -CTGCAGCTCTGG- :::::::: TCTGCAGCCCTGGC 140 2150	T : AAGT	40 2250 TCATTCTCT-TACCCACC- ::::::::::::::::::::::::::::
2100 ccGTGG:::::	: AG(); ; ; ; ; ;) \GAZ	2250 TAC
21 660 :: 601	AGG	170 CTGCAGCT :::::: CTGCAGCC	2210 CA :: .GGCAGA	CTCT ::. GTCA
0 0 0 0	 AGA 70	2170 -CTG :::: TCTG	2 GAG 10	11 11 C C C C C C C C C C C C C C C C C
2090 GGTGGAGTGGC ::::::::::::::::::::::::::::::::::	 AGGAG 2070	217 CT(:: TTTCT(2140	 3AGGA 2210	40 ICATT(.:.:: ACTTT(2280
2090 GGTG(::::			1997	2240 TC : :
GAC	- - - - - - - - - - - - - - - - - - -	- - - - - - - - - - - - - - - - - - -	 (GTJ)	- CC7
2080 CGCCAGCC :::::: TGCCAGCC	-C-TGC- : ::: ACATGCT	-TTCCC- : :: TTGGCCT 2130	 AGGA	 AGGA(
30 3CA 3CA 3CA	3AC	T - 15	 3AA 2	I : 1GA 2
2080 3CGCC 3TGCC		 3AT	CAC	CT :: CCCTGA
2080 2090 2100 2110 2120 2130 GACAGCGCCAGCCGAGGTGGCCGTGGTCCCCGCATCAGGTAATTCTGCCCAAGGCTCA :::::::::::::::::::::::::::::::::::	2140 AC-TGC	2160 TTTCTTCCCCCTGCAGCTCTGGGTCACCTGACCTGTAGTCCTTT ::::::::::::::::::::::::::::::::	2210 2220 2230 H AACCCAC	i Ö
::: 1 GAC 1980	A ATG(2050	2160 TTTC : : GTGC 2120	AAC(: : 1 TCC/ 2190	H GC- :: M GCA 2260
ΗΣ	М 2	HΣ	Ξ	H Z

Fig. 24R

roysors oddand

3-AT : : 3CAG		rcrc :.:	50 FGCA . :.) - 1000 -
TGT(:: TGG(TGA- ::. TGG2	ACA: :: -CA(2450 TATTG ::. GATAT	 3GAC
320 TACCCTG .:::::: AACCCTG 2390	.50 .TCTGTG .:.:: ACAGTG	2390 -CTC	ACC: TTC	 TTGG
2320 L-TAC .:: 3GAAC	2350 -ACCATCTGTGA :::: .::: GACCAGGGACAGTGG 50 2460	2 3 3 3 3 6 7 7 7 7 7 7	10 CATC FIGC	GCT
-CTT :: ACT(ACCA-:::ACCAC	TGT(:::: TGT(2440 CCTCA :: .	ATGC
GCGT GAAA 2380	A(: ATGA(2450	2390 CCTGTGGCTCACATCTC :::::::::::::::::::::::::::::	; GAT,	 ;AGAA 2660
2290 2300 2310 2320CTTGTGG-GTATCTCAGCTCTCCGCGT-CTT-TACCCTGTG-AT : :::::::::::::::::::::::::::::::::::	 36CP	 FGTG	2430 2440 2450 -GCCTCTCCAAGGGTCCTCATCACCTATTGCA :: .: .: .: .: :: .: .: .: .: .: .: .: .	 CAGG
CTC	TGT(i D C	2430 CTCCAA : : : CGCGG	O TAC TGC
0 231 CTCAGCTCTC:::: CTCTGCTCTA	 ATGG'	 TGGG	3CCT 3CTA 3CTA 258	2480 TTCCACTAC ::::::: ATCCGCTGC
2300 TATC	GTCZ	AGA!) EC(2470 2480CTATTTCCACTAC : .: .: .: .: .: .: .: .: .: .: .: .: .:
2 3-GT 3-GT	 rgrg) A FGCA	20 CAG- CGGC	70 CTATT : :: CGTTG
90 CTTGTGG: ::: CAGATGG' 2360	-ACTG :::: AACTGT(2430	2360 2370 2380 -CCCTTCC-CTGCCATTGGGCCCTCCA- :::: :::: :::::::::::::::::::::::::::	2410 2420 GAGCATCCTCAG- : : : : : : : : : : : : : : : : : : :	2470 CT, : TGCCG
2290 CTT ::	A : 1GAA)C : :	SCAT ::	
22 TGGJ	 666 <i>4</i>	6660 . :: ATCO	10 -GAC :. TGG1 60	C CGCZ
, TTGT 2350	.c :: :CTGG	2370 ::: ::: :::2490	2410 G. : ATTTG: 2560	-GCTCGGC- :::::: GCTCAGCG
CCAC:::CTTC	2340 -cccGcc- :::: TccTGTCT	23 3CCP .:::	A : AAAT	- GCT
 : TGA() ::	-CTC	CA: :: :CTCA:	60 .AGG .:: .GGGCT 2620
2280 TCGGATAT :::::. GAGGGTGA	C CTACT' 2410	50 FTCC-(: : FGCAA(2480	CA :: CIGG	2460 CAGG ::: GACGGG
22 ATCTC ::: ATCG2	-CAGC- :::: acagcī	2360 CCCTT::: CCCTG) ::: :::	TT GAG
2280 -CAATCTCGGATATCCAC- : :: :: :: :: :: .: .: .: .: .:) 7 7TGA	 :GTG	3400 2410 2420 2430 2440 2450 GCCAGCCCCACAGAGCATCCTCAGGGCCTCTCCAAGGGTCCTCATCACCTATTGCA	2470 2480GCCTTCAGGGCTCGGCCTATTTTCCACTAC
2280 2310 2320 HCAATCTCGGATATCCACCTTGTGG-GTATCTCAGCTCTCCGCGT-CTT-TACCCTGTG-AT ::::::::::::::::::::::::::::::::::::	2330 2340 H CCCAGCCCCGCCACTG	2360 2370 2380 HCCCTTCC-CTGCCATTGGGCCCTCCACCTGTGGCTCACATCTC :::::::::::::::::::::::::::::	2400 H GCCAGCCC . ::: M AGCTACCC	н М АЛ

Fig. 248

Fig. 241

		2690			2700	
H CGCTTTGT-	I	AAC-	.CD.		CAAAAAAAAAAAAAAA	Ø
•••	••	•	• •			
M CICCIIGICCCICG	TCCCTCGATNI	CGTNAGGGGA	CACTGTGCTA	LTCGATCTT	AINTCGINAGGGGACACTGTGCTATTCGATCTTGATTGTCGAAGAGTTTTTAGGAT	H
3030	3040	3050	3060	3070	3080 3090	
2710			2720		2730	
H AAA		AAAAA	AAAAAAAAGGGCGGCC-	CC	GC	
••		••	•••	••		
M GGAGTAC	M GGAGTACCAGCAAAACCAGGTGGAAATAAAGTTGTCTGAACCCCAAAGAAAAAAAA	AGGTGGAAATA	AAGTTGTCTG	AACCCAAAGA	AAAAAAAA	
3100	3110	3120	3130	3140	3150	

Fig. 24(

11	31.	51 186	71 246	91	111	131 426	151 486	171 546
. J E	G GGA	L CTA	L CIG	G GGA	C TGT	P CCA	S AGT	C TGT
L L CTG CTC	CCC	A GCA	T ACT	D GAT	Y TAC	N AAC	I ATC	F
GCC CT	9 9	T ACA	N AAC	P CCA	K AAG	G GGA	C TGC	C TGC
L Z	CIC	W TGG	Y TAC	N AAT	W TGG	H CAT	TACT	A GCT
CGC C	9 9	N AAC	P CCA	R AGA	Y TAC	D GAT	Q CAA	Y TAT
A GCC C(PCCC	Q CAG	H CAT	C TGC	V GTC	KAAAG	I ATA	9 9
A GCC GC	S AGC	T ACA	Q CAG	Y TAT	GGT	Y TAC	T ACC	S TCA
P ZCC G(PCCT	G	F	N AAC	D GAT	C TGC	CIC	E GAG
CCG CC	A GCG	R AGG	T ACT	H CAC	E GAG	9 9	K AAA	M ATG
A GCG C(P	Y TAT	E GAG	E GAG	H CAC	L	N AAC	999
	R CGG	D GAT	N AAC	GGT	E GAG	N AAC	S TCC	A GCT
CC A	A GCC	A GCG	W	Γ	A GCA	G GGA	TACG	F TTT
CGGC	A GCG	GGT	F	9 9	V GTG	PCCT	K AAA	K AAG
CGTC	L CTG	N AAT	L CTG	999	Y TAT	M ATG	S AGT	TIC
CACG(T ACG	A GCC	C TGT	E GAG	C TGC	Q CAG	TACC	R AGG
מפככנ	L	T ACA	P CCA	999	W TGG	C TGC	g GGC	Q CAG
CGTC	A GCG	F TTC	K AAG	N AAC	P	A GCT	T ACT	S AGT
CACG(A GCG	C TGT	999	P	S AGC	P	L CTA	R CGG
M GTCGACCCACGCGTCCGCCCACGCGTCCGGCCC ATG	A GCC	E GAG	ე ე	Y TAC	V GTG	I ATA	PCCT	C TGT
GTC	S TCC	P	Q CAA	K AAA	D GAC	E GAG	. P	FTTT

Fig. 25A

COVECK CHAROL

Q 1	0 1	Н 9	9	Ч 9	1 9	L 9	9
19	21 66	23	25 78	27	29	31	33
V GTC	T ACT	D GAC	A GCC	E GAG	P CCT	N AAT	R AGG
S AGC	D GAT	P CCT	GGG	V GTG	PCCA	I ATC	E GAG
N AAC	FTTT	S TCC	P	M ATG	R CGC	R GGC	Q CAG
C TGC	L	Y TAT	V GTT	D GAC	s AGC	D GAT	P CCA
E GAA	I ATC	V GTC	R CGG	A GCG	R AGG	S TCT	L CTG
T ACC	I ATC	V GTG	I ATC	S TCG	GGG	F	E
S AGT	R AGG	S	T ACC	D GAC	H CAC	F	E GAA
A GCC	9 9	S TCT	W TGG	R AGG	F TTC	Y. TAT	K AAG
A GCA	D GAT	M ATG	Y TAC	I ATC	R CGC	$_{ m L}$	V GTC
E GAG	9 9	A GCC	C TGC	D GAC	A GCC	I ATC	A GCC
GGG	GGT	S TCA	V GTC	F TTT	L CTA	V GTC	Q CAA
Y TAC	C TGT	Y TAC	R AGG	$_{ m CTA}$	V GTC	F	$ m_{Y}$
K AAG	PCCC	N AAC	G GGG	P	R CGT	D GAC	L TTA
W TGG	Q CAA	GGG	T ACG	F TTC	H CAC	L CIG	V GTT
Y TAC	TACC	G GGT	A GCC	S AGC	T ACC	S TCT	A GCT
D GAT	H CAC	C TGC	Y TAT	F	$^{ m Y}$	V GTC	F TTT
PCCT	D GAT	A GCC	T ACC	H CAC	9 990	N AAC	GGA
N AAT		9 9	D GAC	I ATC	D GAT	F TTC	Q CAG
N AAC	FTC	V GTG	P	H	L CTG	S	A GCC
G GGA	ည ၂	L	F	S TCC	L	L CTG	Q CAG

Fig. 25B

351 1086 391 411 S AGC Q CAG A GCA E GAA PCCT S AGT P CCA R AGA H CAC A GCC S AGC S AGC T ACA A GCC PCCC GGA V GTC S AGC A GCT TACA TACC G GGG L CIC T ACG T ACC M ATG I ATC I AŢC P L GTG GIC P CCA L CTC E GAG Y TAT A GCG TACT A GCC CIC W TGG A GCA V GTC S TCC L CTG K AAA N AAT GGT Q CAG S AGC S ICC Y TAT N AAC S TCC GGT V GTC R P CCA T ACA WTGG A GCT A GCC V GTC GGA P A GCT TACT

431 1326 R AGG LCTT D GAC G GGG S TCA A GCT PCCT V GTT R CGT H CAT S TCC K AAA F TTC T ACA V GTC H CAC L LCTT I ATA K AAG

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PCCC T ACT S TCC PCCT R CGC K AAG $^{
m Y}$ Q CAA I ATT Q CAA S AGC S AGT \overline{W} Q CAG I ATC GGT K AAG E GAA G GGG LCTC S TCG K AAA K AAG TACT G GGG K AAG P CCA F TTT Q CAA I ATC H CAT S TCC $^{\mathrm{C}}$ I ATT D GAT S TCA

DGAC S AGT GTG > L

14

Fig. 25C

1620 1657 AAACCCCACTGTGCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCTGTGGTTCTTCTC TGACAGACTCTTCCCTCTCCCTCTGCCTCGGCCTCTTCGGGGAAACCCTCCTACAGACTAGGAAGAGGCACCT GCTGCCAGGCAGGCAGAGCCTGGATTCCTCCTGCTT

Fig. 25I

79	19	137	39	197	59	257	79	317	66	377
3600	А	D D	Ω	GAT	Z	AAC	ഗ	299	ഥ	GAG
rgac(L 1		Ø	GCA	ß	TGG	Н	CIG	Ø	CCC
3CAC1	T I		ტ	GGT	<u>г</u> ч	TIC	ტ	GGA	>	GTG
rccc	Н		Z	AAC	Н	CTG	ტ	GGA	×	TAC
3666.	Ą		A	GCC	ပ	TGT	⊡	GAA	ပ	$_{ m IGC}$
3000	A 1		Ħ	ACA	വ	CCA	ტ	999	M	$^{\mathrm{TGG}}$
) 9 2 9 1 9 1	A i		Ŀı	TIC	X	AAG	z	AAC	പ	CCI
36600	S		ပ	TGC	ტ	999	വ	CCC	ഗ	AGC
CCCC	ᄓ		ы	GAG	ტ	GGT	≻	TAC	>	GTG
rcrg(ц.		Д	CCC	Ø	CAA	X	AAG	Ω	GAC
ממכנו	Æ		ტ	255	ы	CTG	Ц	CIG	ტ	GGA
CIGC	H		ഗ	TCC	A	909	⊣	ACG	Ω	GAT
GGTG(M		~	SSS	₽	ACA	z	AAC	വ	CCA
ICCC	Ā		щ	CCC	ß	TGG	≯	TAC	Z	AAT
CGGC	A		ტ			AGC		500		AGA
CBCC	Ъ			CCC		CAG		CAT	U	$_{ m IGC}$
CGTC	<u>.</u>		Ø	BDB		ACA		CAG	×	TAT
CACG	A		Д	CCC		GGA		TTC	z	AAT
GTCGACCCACGCGTCCGCCTCCCGGTGCTGCCCCCTCTGCCCCGGGCCGCGCCCGGGGGG			æ	CGG	~	AGG		ACT	H	CAC
GIC	Σ	CA	Ą	၁၁၅	×	TAC	ഥ	GAG	ഥ	GAG

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119 437	139 497	159 557	179	199 677	219 737	239	259 857	279
N AAC	S TCT	A GCT	GGG	GGT	S TCA	V GTC	FITT	L CTG
G GGA	T ACC	FTT	H CAC	C TGC	$^{ m Y}$	R AGA	L CTG	V GTC
P	K	K	K	CCC	N		T	R
CCT	AAA	AAG	AAG		AAC	9	ACC	CGC
M ATG	S AGT	F	W TGG	Q CAG	GGG	T ACT	F	H CAC
Q CAG	T ACC	R AGA	YTAC	T ACG	GGT	A GCC	N AAC	T ACC
C		Q	D	H	C	Y	F	YTAC
TGC	GGC	CAG	GAC	CAC	HGC	TAC	TTC	
A	T	S	P	D	A	T	H	9
GCC	ACG	AGT	CCT	GAC	GCC	ACC	CAT	9
P	L	R	N		9	D	I	D
CCT		CGG	AAT	GGG	9	GAC	ATC	GAC
I ATT	P	C TGT	N AAC	F TTC	V GTG	P	R CGC	$_{ m L}$
E GAA	P CCT	TTC TTC		C TGC	L CIC	F	S TCT	L CTG
C	P	S	C	V	TACT	D	A	E
TGT	CCA	AGC	TGT	GTC		GAC	GCC	GAG
YTAC	N	I	F	S	D	P	G	V
	AAC	ATC	TTC	AGT	GAC	CCT	GGA	GTG
K	G	C	C	N	F	S	P	MATG
AAG	GGA	TGT	TGC	AAT	TTT	TCC	CCA	
WTGG	H CAT	T ACC	A GCC	C HGC	CIC	YTAC	V GTT	D GAC
Y	D	Q	Y	E	I	V	R	A
TAC	GAT	CAA	TAT	GAG	ATC	GTG	CGG	GCA
V	K	I	295	TACC	I	V	I	S
GTC	AAG	ATA	GGC		ATT	GTG	ATC	TCT
G GGA	YTAC	T ACC	S TCA	S AGC	R AGG	A GCC	TACC	D GAC
D	C	L	E	A	295	A	WTGG	R
GAC	HGC	CIC	GAG	GCC	GGC	GCA		AGG
E	ე	K	M	A	D	M	Y	I
GAG	ცცე	AAG	ATG	GCG	GAC	ATG	TAC	ATC
H CAT	L	N AAC	999	E GAG	999	A GCC	C TGC	D GAT

Fig. 25F

359 1157 419 439 379 399 459 1457 319 339 299 977 1097 O CAA R AGG S TCC ATA R CGT LCIC E GAG E GAG H CAC CCC S TCA Y TAT N AAT A GCA G GGG GAT $_{
m ITG}$ LCTC R CGA L TTA L CTG S AGC $_{\rm L}$ L CTG R AGA V GTG V GTC PCCT W TGG H CAT LCTT T ACC K AAA I ATT A GCC S TCA G GGG R AGA S TCT A GCT Q CAG S TCC A GCC T ACG M ATG $_{
m L}$ F TTT N AAT GGA N AAC S TCC V GTA CTGT C S AGC S TCT ·F TTC Q CAG V GTC H CAC Q CAG L FTTC V GTC P CCA A GCC A GCC A GCC GGA $_{
m F}$ S TCT A GCT S TCT L CTG Q CAG PCCT TACT D GAT R AGA TACT Q CAA A GCT L CTA Q CAG K AAG Q CAA G GGG PCCT N AAT R AGA S AGC P E GAG S TCG I ATC V GTC PCCG W TGG $_{
m LTA}$ P CCA TACC Q CAG E GAG L ITG R S AGT LCTT R PCCT S AGC D GAT P CCA L H CAC T ACA Q CAG E GAG N AAC M ATG R AGG PCCG N AAC S AGC A GCC Q CAG Q CAG S TCT G GGG A GCC P CCC S TCA E GAA T ACA H CAT S TCT FITC E GAG Q CAA PCCA Q CAG L CTG S AGT F TTC S AGC FTTT LCTC K AAG E GAG P G GGG S TCA S TCC P CCA Y IAT TACC T ACC TACC $_{
m L}$ G GGA R $_{
m L}$ S TCC E GAG V GTC I ATT A GCC I ATC IATC Q CAG S TCA I ATC S TCT

Fig. 25G

A STTTGCTCCCTGAGTT AGAGGCAGCCCAGCCTG TGACAGGACACAGCTGG STTTTCTTTTTGTCCAA SGTTTTCTAGGCTGGCC SCTTTCTTAGGCTGGCCAA AGAGGGTTCTTTTTAGT AGTGAACTTCCTGGATA	GTC AGA GTC AAC AAG ATG ACC. GCA ATC CCC TCG TGA GTGACTGAAGCTCCTCTCTTTTGGGAGCTCCCAAGCTTTGCTCCCCTGAGTTCTCCTCCTCTCAACAACA GTGACTGAAGCCCACGCCTGCATGATGAAGAACACCCTGATTTAGAAGACACCCAGCCTGGATCCTCCATCAACACA GTACCAGCCTGCTTCTGCTGCTGTAAGATTTCTTTGTTTTTTTT
G CLIPE G G	C. GCA ATC CCC TCG TC AGGCTCCGCTCCAAGCTCGI ATGGTAAGACAGGCCCAGGC TAGGATGAAAGAACTGTCI AGGCCCAGTGTAGGATCTTCI AGGCCCAGTGTAGGCTTGGI ACACCAGATGTCATCTTTCI TTTGTCCATGGAACTGCCTCGI TGGAATCAGAATTCAGCCTC

Fig. 25H

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4928	THCTHCTACADADADADADADADADADACGCCCCCC
489(AATGGAATGTGATGGTACTTAACTTTTACAAAAGAGAGAAAATGTTATTTTTACTGTTTGAAGAAAATAATTTTCTCA
4813	TGTATTTTAAAATATAAAATGAAGTGTGACACACTGTATACAATTTAATATATAT
4732	GGATATGACTTTGGACAACAAGGCTTTATTTGTAAATATGCTCTTAATATGCAACTTTGAGAATAAGATAGAAACATCA
4653	AGAICCAGCGAGGGAGCIGCCAICCCCGCCACCIICAIAGCAGCAAGACCIICCCAITICCAAICICACCTCCAGCAG
457	ACACTGGCCCAGGCTGAGTGGGCCAGAGCAACAAGTGGAAGGGGATCTCTCTC
4495	GGCTGCACCCCCACCCTGGTCTGCCAACAGAACCTGGGGGCCTCACACGGGCTCCTGTCTTGCCAAGCTGGAGCTGAGC
441	GICTCTGTTTACTGTCCTCTTCTACCTCCAGGTCACTTAGCTCTGGCTGCTCTGGCTGG
433	GIGGAGIGICCIGITIGAIGICIGAGGICIGCITIGGGIACCGCCCIGGGAACIGCIAACCICCGAIIGGICCCIIIGI
4258	CTCTGTCAGCCTCTGCAGGGGCCACACAAGTCTCCCGAGCCAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCTCCT
417	GAGCTCGCGCCCGGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA
410(GIGCCACCCCACGGCICACIGICATCCCAGGAGGGACCCCCACCIGATGCICCTCATCATCGCTGGCCTGACACTAICA
402	AAAGCTCTTGAAGATCAAAGCTCTGGCGGGTACAGCTGTCCTGGCCTGTGGGCCCAGCCCATGGGATGTGCCTGGGCCAG
3942	GCGGCTGCCTAAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA
386.	TCCTGTCACACTGCTTACAAAGCAGAGACAGAGTAGGAAAGAGGTCTTCATCCTCTCCCACACATCAGCAAGGATAGGGCT
378	GAGCATAGGGGTAAGCCGAGGGAGAAGAGCAGCCCTCAGAGACATCAGCTAAAAAACATAGGTGCCCTATGTCCCTCCC
3705	CAGAAATGACAGGCACAGTCTGTTAGAACCTGTAGGCAGCCAGTCACAGAGGGCCTTTGTGCTGGTAACACCCTGCCTG
362	ATAAGGAAAACTAACCCACCTCCAACAACAGCAGAGGACAGTGGGAAGGAA
354	TGCCCACGCTCCTTTTGCTGTGGGCCTGGCACAGCCCAACACTGCAGGGCCCCACCTTCTCTTTGGGGGGTAGGGACAC
3468	ATCTCGGACACAGGAAGCAAGCCCCCAGTGTGGTGGCAGCTGCGGCTCAGCATTGGTGTCCCCCAGGAAGGGCCGGTGGATG
338	ATAGCAGGCCAGGACATTTTTTCAGCTCAGAGCACTGGCCCCCAGGCTTCCTCTAAGCCACCACTCACCTGTCTTCCT
331(CCCTGAGACCAAGTGTTGAGTCACAGAGTGCCCATGTGCGTAGTGCATAAAGGATATGGGTTCTTAACCAGGGAAGGCTC

Fig. 25

10 50 70 Hum. MAPPAARLALLSAAALTLAARPAPSPGLGPGPECFTANGADYRGTQNWTALQGGKPCLFWNETFQHPYNT ::::::::::::::::::::::::::::::::::::	80 100 110 120 130 140 LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEIPACQMPGNLGCYKDHGNPPPLTGTSKT :::::::::::::::::::::::::::::::::::	150 160 200 210 Hum. SNKLTIQTCISFCRSQRFKFAGMESGYACFCGNNPDYWKYGEAASTECNSVCFGDHTQPCGGDGRIILFD ::::::::::::::::::::::::::::::::::::	220 230 240 250 260 270 280 280 280 280 270 280 210 280 210 280 210 280 210 280 210 280 210 280 210 220 230 240 250 250 250 270
10 20 MAPPAARLALLSAAALTLAARPAP :::::::::::::::::::::::::::::::::	80 90 LKYPNGEGGLGEHNYCRNPDGDVS ::::::::::::::::::::::::::::::::::::	160 SNKLTIQTCISFCRSQRFKFAGME ::::::::::::::::::::::::::::::::::::	220 230 TLVGACGGNYSAMSSVVYSPDFPD ::::::::::::::::::::::::::::::::::::
Hum. MA::: Hur. MA	Hum. LK :: Mur. LK 70	Hum. SN: :: Mur. SN:	Hum. TL :: Mur. TL

Fig. 25J

OOFEDIEL CITEDI

350	ZANLSV		ZANLSV		420	LHVTFK		DRFFCM	410						
340	QTVAEVITE	•••	OTLAEVITE	340	410	VTAIVAKIL	:	SSSOSOOTS				D	•	S	0
330	LPQERPAVN	••	PPQERPAVN	330	400	GLATLLILT		-GLCTAWRPS	400	7	7.7	-QDDRNPLVS	:	/RVNKMTAIP	470
320	AVLYQAVKEE	••••••	AVLYQATKEE	320	390	SHRVEGWTV		ATEWKD-	390		400	KKKLKGQSQ-	:	SPSLRRSSRV	460
310	SDRINQAQGE		SDRINQAQGE	310	380	ISWAPPMGAG		PGHRQLGPT.	380	- -	400	KPSTSISIE	•	SPESMNLPLO	450
300	LDFVILYFFS	••••••	LDFVILYFFS	300	370	HPPQTVPGSN	•	HPPQTAQVA]	370	0	440	TSGEIWSIE	••	VSLGLLEISC	440
290	LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFAVLYQAVKEELPQERPAVNQTVAEVITEQANLSV	••••••••••••••	Mur. LVRLSGRSRPPLSFNVSLDFVILYFFSDRINQAQGFAVLYQATKEEPPQERPAVNQTLAEVITEQANLSV	290	360	Hum. SAARSSKVLYVITTSPSHPPQTVPGSNSWAPPMGAGSHRVEGWTVYGLATLLILTVTAIVAKILLHVTFK	••	Mur. SAAHSSKVLYVITPSPSHPPQTAQVAIPGHRQLGPTATEWKD-GLCTAWRPSSSSQSQQLSQRFFCM	360		4.50	SHRVPASGDLRDCHQPGTSGEIWSIFYKPSTSISIFKKKLKGQSQ-QDDRNPLVSD		SHINLIESLHQETLGTVVSLGLLEISGPFSMNLPLQSPSLRRSSRVRVNKMTAIPS	430
	. LARFHGR		. LVRLSGR	280		. SAARSSK		. SAAHSSK	350				••		420
	Hum.		Mur			Hum		Mur				Hum.		Mur.	

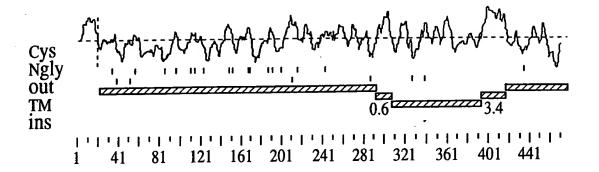


Fig. 25L

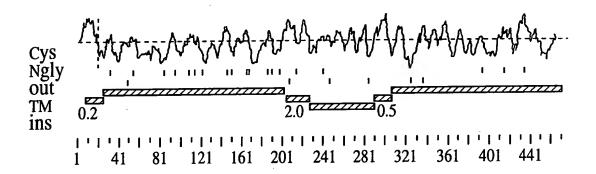


Fig. 25M

13		126	53		73	246	93		113	9	\sim	426	153 486
G GGA	Z	AAT	ტ	GGA	ပ	\mathtt{TGT}	Ĺτι	$_{ m LLL}$	Ω	GAT	ტ	GGA	L CTG
F TTT	ц	CTG	Z	AAT	>	\mathtt{GTG}	പ	CCA	ᆸ	CLL	M	${ m TGG}$	N AAT
D GAT	н	CIC	>	GIC	₽	ACT	U	\mathtt{TGT}	M	$^{ m LGG}$	闰	GAA	A GCC
I ATT	ы	CIG	ᆸ	CIG	ტ	GGG	ტ	GGA	Н	ATT	· 44	SSS	E GAA
H CAT	н	ATC	ద	AGG	M	TGG	Ц	CLL	云	AAA	н	CAC	G GGT
W TGG	ပ	IGC	ᄓ	${ m TTG}$	Ø	CAG	Ø	CAG	ტ	GGA	Ø	CAA	Y TAT
S TCG	⊟	ACT	ഥ	GAG	ტ	GGA	又	AAA	H	CAT	U	\mathtt{TGT}	C TGT
N AAC	>	GTA	Ц	${ m TTG}$	Ø	CAG	ပ	IGC	ĸ	AGA	⊡	GAA	N AAC
Q CAA	>	GTG	Ω	GAT	Ĺτι	$_{ m LLC}$	>	\mathtt{GTG}	₽	ACT	M	IGG	V GTG
PCCT	Ą	GCT	₽	ACA	X	AAA	>	GIC	\triangleright	\mathtt{GTG}	Ы	CIC	G GGT
L CTG	S	TCT	ധ	GGA	>	$_{ m GIG}$	E→	ACT	A	CCC	A	GCT	V GTT
M ATG	ĮŦi	TTC	Z	AAT	闰	GAG	ഗ	TCA	Ø	CAA	ഗ	TCA	D GAT
M ATG	н	CTT	দ্য	$_{ m LLL}$	>	GTG	A	CCC	ტ	GGA	ഥ	GAG	E GAA
AGTA	Z	AAC	ഗ	AGT	₽	ACA	₽	ACT	Ĺτι	$\mathtt{T}\mathtt{T}\mathtt{I}$	Z	AAT	G GGA
AACTA	Ø	CAG	ഗ	AGC	ტ	GGG	H	ACT	ፚ	CGT	ט	GGA	H CAT
TAG	. ==	CAT	H	ATC	S	TCT	Z	AAC	Гт	TTT	×	TAT	$^{ m Y}$
GATC	U	TGT	ц	CIC	ပ	TGC	M	$^{ m LGG}$	Σ	ATG	U	\mathtt{TGT}	C TGT
STCGC	ပ	TGC	ᅜᅺ	TTT	Д	CCC	ტ	GGG	A	CCC	ഗ	TCC	N AAC
GCGCCCCTCGCGATCTAGAACTAGTA	Ŋ	IGC	Ö	IGC	ტ	GGT	Ω	GAT	ഥ	TTC	>	\mathtt{GTT}	H CAT
9929	K	AGA	ഗ	ICC	Ω	GAC	Ω	GAT	ഗ	ICI	Ω	GAT	S AGC

Fig. 26A

173 546	193 606	213	233	253 786	273 846	293 906	313 966	333 1026
Q CAA	C TGC	V GTA	N AAT	T ACT		N AAT	GGC	GGT
F	V	A	W	L	M	N	A	S
TTC	GTG	GCT	TGG	TTA	ATG	AAC	GCT	TCC
K AAA	V GTG	PCCT	L	T ACA	C TGT	W TGG	F	C TGC
V	A	S	A	V	R	K	H	S
GTG	GCC	AGC	GCA	GTC	CGC	AAG	CAC	
E GAG	A GCT	N AAT	Γ	D GAT	N AAC	H CAT	L	V GTC
V	T	V	E	E	T	H	A	GGT
GTG	ACT	GTT	GAG	GAG	ACT	CAC	GCA	
R	N	V	N	N	G	C	TACC	D
AGA	AAT	GTT	AAT	AAT	GGA	TGC		GAT
GGG	L TTG	G GGA	G GGG	H CAC	GGT	V GTA	G GGA	L
S TCA	N AAC	S	Q CAG	S AGT	V GTA	TACC	C TGT	W
C	W	S	C	C	L		G	V
TGT	TGG	TCT	HGC	TGC		GGG	GGA	GTA
S TCC	G GGG	I ATT	$_{ m L}$	D GAC	R AGG	W TGG	$_{ m ITG}$	V GTT
N	D	FTT	I	H	L	R	Q	D
AAC	GAT		ATT	CAT	CTA	AGG	CAG	GAT
N	D	S	D	N	E	G	K	S
AAC	GAT	TCT	GAC	AAT	GAA	GGA	AAG	TCT
G GGA	C TGT	S	D GAT	G GGA	L	Q CAA	C TGC	GGG
D	I	P	L	W	D	I	V	S
GAT	ATA	CCA	CTG	TGG	GAT	ATC	GTA	TCA
V	T	C	W	G	S	K	V	Q
GTG	ACT	TGT		GGA	AGT	AAA	GTC	CAG
L	G	G	I	R	S	L	D	$_{ m ITG}$
CTA	GGG	GGA	ATT	CGT	AGT	CTG	GAT	
R	W	L	PCCC	H	D	E	A	H
AGG	TGG	CTA		CAT	GAT	GAG	GCT	CAT
L	R	Q	R	R	Y	V	A	PCCT
TTG	AGG	CAA	CGC	AGA	TAT	GTA	GCA	
GGT	E GAA	R AGG	L TTG	C TGC	C TGT	R AGA	A GCT	Γ

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Fig. 26B

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L4 LU

1326 453 1386 393 1206 413 353 086 373 433 1446 506 493 I ATA PCCG I ATA H CAT GAT K AAA GAT TAC Ω \Box A GCA ACA W TGG GGA A GCA LCTT K AAA $^{\rm C}$ \vdash L CTA TGG GGA K AAG GTG $^{\rm C}$ I ATT GAT 3 \Box > W TGG D GAC E GAG D GAC R CGA L CTA ${
m Y}$ TAT D GAT L CTG Q CAG Q CAG R AGA ACA $_{
m L}$ FTTT S TCT \vdash K AAG E GAA E GAA C TGC R AGA N AAT $_{\rm TGT}^{\rm C}$ A GCT $_{
m L}$ $_{
m TGT}$ E GAA D GAC I ATT GGG H CAT G T ACC W TGG V GTA D GAT I ATT V GTT N AAT TAT \succ GGA A GCA R AGA V GTG LCIC GGA S AGT $^{\mathrm{C}}$ Ŋ S TCC GGA GTG L A GCT P CC C PCCT A GCT \gt E GAG A GCC K AAA S TCA H CAT D GAT D GAT S AGC R AGA S TCA V GTA Q CAA A GCT E GAG S TCA H CAT C E GAA R AGA C TGC R AGA N AAT A GCT R CGT G GGG D GAC I ATC N AAT G GGG R CGA GGG R CGT W TGG V GTG S TCA K AAG $_{
m ITC}$ T ACT V GTC S AGT \overline{W} GGC C TGC C TGC LCTT LCIT S TCT $_{\mathrm{TGT}}$ V GTG T ACA R AGG FTTTN AAT N AAC F TTT S TCT Q CAG L CTA D GAT N AAC V GTC I ATA R CGA S TCT D GAC K AAG GAA N AAC S AGC S AGC D GAC S AGT 冝 A GCA $_{
m L}$ N AAT Q CAA G CTGT F TTC N AAC

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Fig. 26C

513566

GIG

GTT

A GCT

GCA

AAT

ACA

R AGG

S AGC

WTGG

D GAC

H CAT

CTGT

V GTG

T ACT

GGG

W TGG

E GAG

GGA

CAA

K

AGA

 \gt

ø

Z

 \vdash

613 1866 533626 553 593 806 633 .926 986 673 2046 693 2106 653 686 E GAA W TGG S TCG V GTA N AAC M ATG GAT S AGT \Box K AAA I ATC I ATT C TGC TGG 9 CTGT C LCTT 3 GTG TTTAAT GGC I ATT AGG R CGC TCC GAC \gt Ç Ω α Z S TAT S TCA GAT N AAC GAC IATC AAT L CTG GTT Ω \Box \mathbf{z} GAG GAG GAG S AGC D GAT GAT AAT S TCT 团 回 Ω 闰 Z ATG AGA 9 GGA ATG N AAT $^{\rm C}$ S TCT D GAT α G Σ GGA CAC GGC GTG PCCA L CTC TGG GAT GGT G G н Ŋ \gt \geq \Box GTA S TCG VGTG T ACA \overline{W} GGG F TTT I ATT C \triangleright G GCA C TGC $^{\rm C}$ L CTG GGC GAC I ATT AGT ᠐ Ω S Ø R AGG W TGG $_{
m CTG}$ K AAA AAC N AAT GAT CAT S TCT \Box Z ATG Q CAG GGA AGG GTT CAT L CTG R CGG TCT \gt 耳 G α S D GAC K AAG GGC CCT GGA S AGC Y TAT C TGC $^{\mathrm{C}}$ AAG I ATC GGA \overline{W} Q CAA D GAT GGA TCA TGT G \mathcal{O} G ഗ GGA GTG Γ W TGG T ACA GTG T ACA W TGG F TTT > G A GCA Y TAC GTG GGA W TGG GGA S TCT L CIC TGT \mathcal{O} G \gt G D GAT V GTG GGA I ATT S AGT A GCT 'A GCT D GAT GIT > $_{
m ITG}$ CAC E GAG GCA N AAC TCA GAT PCCT GGT 田 Ø ഗ Ω E GAA Q CAA EGAA S TCA L A GCT G GGA E GAG GGA K AAA L CTG AAA S TCA TGT C TGC R AGA D GAT AGT \searrow \mathcal{O} S DGAC T ACC G GGA H CAC A GCA GGA S AGT GGT $^{\rm C}_{
m TGT}$

Fig. 26D

793 773 813 2466 733 753 286 873 222 252 258 E GAG R AGG L TTA A GCA G GGG $^{\rm C}_{
m TGT}$ C TGC GGA E GAA I ATC W TGG H CAC $_{
m L}$ A GCA K AAA H CAT Ŋ H CAC A GCC K AAA GTG G GGA LCIT R CGA LCTT A GCC L TTA I ATA S TCA V GTG H CAC o CAA N AAT $^{
m F}$ R AGG T ACA $^{\rm C}$ C TGC E GAA A GCC H CAC TACT GGT Q CAG C TGC R AGA D GAT IATC E GAA V GTT A GCT D GAT W TGG V GTT GAA L TTG R CGT H CAT GGA S AGT Ŋ ഥ T ACA G GGG L GGA GTG N AAT S AGT LCTT V GTT \gt GIG A GCA E GAA E GAA $^{\mathrm{F}}$ S TCT S TCT S TCT S TCT E GAG A GCC E GAA C FTC $^{\rm C}$ A GCT H CAT LCTT Q CAG M ATG I ATT E GAA P D GAT P CCT S TCT M ATG K AAA N AAC E GAG GGG N AAT S TCT I ATA F TTC M ATG A GCC K AAG R AGA GGA L TTA D GAT D GAT GGA E GAA A GCT GGA S TCC TACT H CAT A GCT $_{\mathrm{TGT}}^{\mathrm{C}}$ D GAT W TGG V GTC GGA GIC GGA A GCC $_{\mathrm{TGT}}$ C TGC $^{\rm C}$ G \gt W TGG R AGG R AGG A GCG GGC GGC V GTT $_{\mathrm{TGT}}^{\mathrm{C}}$ S TCT IATC L CTG N AAT T ACT S AGC N AAT S TCT TACT R L CTA A GCA N AAT Q CAG R AGG W TGG L TTA S AGC A GCT S TCG T ACA GGA K AAA P CCC E GAA CS TCT GGT G G GGT L CTG G GGG MATG W TGG Q CAG D GAC R AGA N AAT

Fig. 26E

893 3008 2946 3186 933 826 953 886 973 993 282 288 1013 312 E GAG GAT K AAA AAT AAT GAC CAC \Box Ω Z \mathbf{z} 田 E GGA GGA E GAG CAA A GCA N AAT \mathtt{TAT} G GGG GGA G GGG CCA GGA CAT LCTC L TTA G G Д Ξ D GAC D GAC T ACA I ATC GAG L TTA C TGC C TGC 囝 GAA W TGG ACC $^{\rm C}$ CCA I ATC $^{\rm C}$ TGT Ö [고] \vdash Д \gt R AGA Q CAG H CAC S TCA $_{
m ITG}$ R AGA H CAT PCCC F TTT S AGC S TCC TACC LCTC F TTT PCCT L CTG A GCT . GGG CAC D GAC R AGG A GCC K AAA A GCA P CCA A GCT S AGT I ATC GGC H CAC Q CAG GGC C TGT TACT GGA $_{\mathrm{TGT}}^{\mathrm{C}}$ G G G L CTG G GGG GGA T ACC E GAG R CGC $^{\rm C}$ N AAT LCTT GTG TGG $_{
m L}$ CCA S AGC ACT S TCA TGT GTT > \mathcal{O} Д 3 \gt GAC LCTT G.G G.G S AGC GTG T ACA S AGC V GTT D GAC \Box \triangleright M ATG GGG GAA W TGG L GGA A GCA CGA R CGT α G 되 Ü PCCG V GTC H CAC Q CAG Q CAA T ACA D GAT GTT S TCT \gt $\frac{L}{TTG}$ GTG CAT GAT G GGA R AGA TGC S AGT $_{
m TGT}$ 田 \Box \mathcal{O} \gt \mathcal{O} L CTA Q CAA T ACA R AGA N AAC I ATC Y TAT C TGC L CTT V GTG GTG CCA TAT L CTA E GAA D GAT R CGC GTT \gt \gt \succ Ω GGA L CTG L IATT R CGA N AAC V GTT S TCT D GAC G I ATC GIC R P S TCC R CGT I ATT L CTT S TCT \gt C TGC $_{
m IGT}$ E SAG A GCC Y TAT S TCA TACT V GTA K AAA

26F

Fig.

3606 1093 V GTC E GAG W TGG A GCT T ACC S AGC S AGC PCCT G GGG I ATC S TCC G GGG $\frac{L}{\text{ITG}}$ V GTC CTGTC TGT H CAC H CAC A GCA S AGC N AAC Q CAG FTTT GTT A GCC S TCC D GAC E GAG R AGG R AGA H CAC G GGA I ATT GAT A GCT E GAG E GAG T ACA R AGG D GAC R CGA N AAT S AGC T ACG K AAG E GAA 9 99C E GAG E GAG D GAT S TCT L CTG V GTC GGA H CAC T ACT GTC G GGG V GTG $\overline{\mathbf{W}}$ D GAC R AGG E GAA W TGG P CCA TACG T ACA S AGC $_{\mathrm{TGT}}^{\mathrm{C}}$ M ATG A GCC W TGG A GCC C TGC C TGC 9 9 9 9 GGC S AGT 9 9 N AAT N AAC D GAC $^{
m Y}$ W TGG L CTG F TTC S TCT $_{
m L}$ Q CAG D GAC L CTG L TACC FTTC H CAC GGT Q CAG R AGG G GGG R AGG D GAT A GCC D GAC S TCT C IGC G GGG $_{
m L}$ N AAC Q CAG C TGT V GTG D GAT C TGC G GGC I ATC L CTG $\overline{\mathbf{W}}$ GGA A GCC Y TAT V GTG T ACA W TGG I ATA TACC W TGG GGC T ACA F TTC K AAG CTGT I ATT I ATC S TCC 9 9 9 9 9 9 9 9 R CGC F TTC V GTC GGC S TCT W TGG L P S TCC E GAA E GAA A GCA L TTA IATC H CAT F TTC K AAG G GGG S TCA L TTG I ATA PCCT PCCT S TCA T ACG R AGA A GCC GGC Q CAA C TGC C TGC A GCC Q CAG I ATC G GGG T ACA K AAA D GAC C IGI G GGG LCTC

Fig. 26G

1393 4206 3968 1333 4026 4086 1313 ATG GAC L CTG L CTG S AGT L CTG LCTC T ACC \Box Σ D GAC E GAG D GAT Q CAG S TCA L P A GCT GGA M ATG GGA GAT K AAA L CTG CTGT S TCT LCTT G Ω G E GAG $_{
m ITG}$ L CTG GGA 9 990 W TGG L H CAT G W TGG P CCC G GGG T ACA S TCG K AAA CGT $^{\rm C}$ H CAT V GTG 9 96C 9 96C I ATC K AAA Q CAG Q CAA F TTC F TTT R AGA W TGG L CTG T ACC A GCC GGA I ATC K AAA L TTA G Q CAG GGA Q CAG S TCC H CAC N AAT S AGT S TCT E GAG AGA Q CAG S TCC 9 66C TACT CTGT C TGC GAT A GCA GGA DGAC R AGG E GAG $_{\rm TGT}^{\rm C}$ L TTA R CGA W TGG GTG L GAA H CAC Q CAG I ATT C TGC ഥ \gt W TGG GTG GGC L CTA 9 96C W TGG L S TCT TGT \triangleright I ATC ACA E GAA A GCA T ACG F TTT A GCT GGT FTTT I ATC E GAG A GCG S TCA D GAT R AGG S TCG $_{
m LTA}$ L TGG E GAG E GAG E GAA R AGG V GTG H CAT A GCT F TTT 3 R AGA ACC A GCC D GAC N AAT K AAG L CTA R AGA GGT H E GAG G GGG $_{\rm L}$ R AGG GGA S TCA T ACC H CAC I ATT G S TCA E GAA D GAC L CTG K AAA GGA S TCT S TCC FTTT WGCA A GCC C TGC A GCC $_{\rm CTG}$ TGC $^{\rm C}$ GTT Ø \mathcal{O} \gt R AGA PCCA E GAG S TCC A GCT R CGG D GAC N AAT V GTT

Fig. 26H

4468

1433 4326	1453 4386	1454 4389
	K	
N H G AAC CAT GGT	T ACA	
N AAC	A GCC	
CCC	E GAA	
T ACC	S TCT	
	A 3CC	
S D D TCA GAT GAC	CCT	
S TCA	L CTT	
T ACC	V GTT	
R T AGA ACC	G GGA	•
T ACA	L TTG	
999	L CTG	
H G CAT GGG	S TCG	
P CCA	T ACA	
D GAC	D GAC	
E	S AGC	
K R E AAG AGA GAG	A GCT	
K AAG	D GAT	
L	C E IGT GAA	
င္ပင္သ	c lgT	* rga

AGTCAAGTTGCCCTATGGAAAACTTGTCCAAATAACATTTCTTGAACAATAGGAGAACAGCTAAATTGATAAAGACTGG CITIAGACTICCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACAACAACTTTTAAATGAATAAAGAGGA

Fig. 26

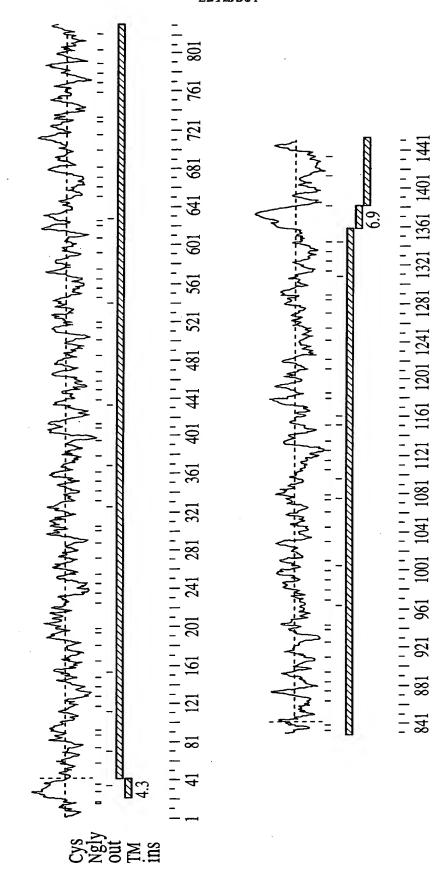


Fig. 26J

<u>oorsolan of appa</u>

Hum.	10 20 30 40 50 50 70 70 70 Hum, MMLPONSWHIDFGRCCCHONLFSAVVTCILLINSCFLISSFNGTDLELRLVNGDGPCSGTVEVKFOGOWG	20 CCHONLFSAVV	30 TCILLINSC	40 FLISSFNGT	50 DLELRLVNGDG	60 PCSGTVEVKFOG	70 OWG
WC1	. : : : : : : : : : : : : : : : : : : :	: . HLSLRGL	-CVLLLGT-	: MVGGQ	ALELRLKDGVE 30	: .: . : .: .: .: .: .: .: .: .: .: .: .	EWG 50
Hum. WC1	80 100 110 120 130 TVCDDGWNTTASTVVCKQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQHREWGSHN:::::::::::::::::::::::::::::::::::	90 CKQLGCPFSFAN :.:::: CRQLGCGAAIG- 70	100 MFRFGQAVT : : ;-FPGGAYFG	110 :R-HGKIWLD :::: ;PGLGPIWLL	110 GKIWLDDVSCYGNESALWECQH : ::: .:::: GPIWLLYTSCEGTESTVSDCEH 90 110	130 JWECQHREWG .:.:	SHN •••
Hum. WC1	140 150 um. CYHGEDVGVNCYGEAN :::::::: WC1 YNHGRDAGVVCSG 120 130		160 170 LRLVDGNNSCSGRVEVK: .::.::::: VRLAGGDGPCSGRVEVH: 140 150	180 (FQERWGTICD) : : : : ISGEAWIPVSD()	180 190 20 DERWGTICDDGWNLNTAAVVCRQLGCP : : .:.::.::::::::::::::::::::::::::::	160 170 180 190 200 LGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSSFISSG .::.::::::::::::::::::::::::::::::::	SSG : VLG
Hum. WC1	210 220 230 240 250 260 270 VVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDSSDLELRLVGGTNRCMGRVE	230 ILCQGNELALWNCRH : :::: ::: : FRCEGEEPELWVCPR	240 INCRHRGWGNI : IVCPRVPCPG(250 IHDCSHNEDVT: : :	260 TLTCYDSSDLEJ : : \QVVCSAYSEVR	230 240 250 260 270 LCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDSSDLELRLVGGTNRCMGRVE :::::::::::::::::::::::::::::::::::	RVE .:: QVE

Fig. 26K

280 330 340 LKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGT :: .: .: .: .: .: .: .: .: .: .: .:	350 360 410 VNFDCLHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSV :::::::::::::::::::::::::::::::::::	420 430 440 450 460 470 480 FGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVGAHSPCY :.::::::::::::::::::::::::::::::::	490 520 530 550 um. GRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE :::::::::::::::::::::::::::::::::::
280 290 LKIQGRWGTVCHHKW .::::::::::::::::::::::::::::::::::::	350 360 VNFDCLHQNDVSVI .::::::: GGPDCSHGNTASVI 330 330	420 430 FGSRRAKPSNEARD :: SQPTGSA	490 500 GRLEVKYQGEWGTVC :::: ::::: GRVEILDQGSWGTIC 390 400
Hum. WC1	Hum. WC1	Hum. WC1	Hum. WC1

Fig. 261

	560	570	280	590	009	610	620
Hum.		VHREDVIV	TCSGDATWGI	RLVGGSNRCSG	RLEVYFQGRW	HSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDC	AAAVVCSQLDC
WC1		: .:.: RHKODAGV	 VICSEFILAI	AI,RMVSF,DOOCAG	DOOCAGWI, FV FYNG TWG SVCRNI	· · · · · · · · · · · · · · · · · · ·	TVSTICEOLGC
) :		470	480	490	500	510	.520
	630	640	650	099	670	680	069
Hum.	PSSIIGMGLGNAST.	GNASTGYG	KIWLDDVSCI	GDESDLWSCRN	NSGWGNNDCSH	GYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGS	DMELRLVGGS
WC1		VALREGFR	POWVDRIQCE	KTDTSLWQCPS	DPWNYNSCSE	-	<pre><qirlvdgg< pre=""></qirlvdgg<></pre>
	530	540	550	560	570	280	590
	700	710	720	730	740	750	760
Hum.	SRCAGKVEVI	NVQGAVGI	LCANGWGMNI	IAEVVCRQLECG	SAIRVSREPH	SRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASL	ISGCTGGEASL
	•		:		:	::	•
WC1		LDQGSWGTI	ICDDRWDLDI O	DDARVVCKQLGCG)	EALDATVSSF	GRCSGRVEILDQGSWGTICDDRWDLDDARVVCKQLGCGEALDATVSSFFGTGSGPIWLDEVNCRGEESQV	VNCRGEESQV
		5					
	770	780	190	800	810	820	830
Hum.	WDCIRWEWK	QTACHLNM	EASLICSAHF	QPRLVGADMPC	SGRVEVKHAD	Hum. WDCIRWEWKQTACHLNMEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCREL	HAANVLCREL
	••••••	•	•	•••••••••••••••••			•••
WC1	WC1 WRCPSWGWRQHNCN		DAGVICSGF-	VRLAGGDGPC	SGRVEVHSGE	HQEDAGVICSGFVRLAGGDGPCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAEL	PTAQVICAEL
	0.19	089	0	7 069	7007	710 720	730

Fig. 26M

Hum.	SVG	850 DHFGKGN	860 GLTWAEKF(870 QCEGSETHLA	860 870 880 890 900 KGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLV-NG	890 TCIHSREVG	900 VCSRYTDVRI	N-NG
WC1	GCGKAVSVLGHMPFRESDGQVWAEEFRCDGGEPELWSCPRVPCPGGTCLHSGAAQVVCSVYTEVQLMKNG 740 750 760 770 780 790 800	: MPFRESD	.: .::: DGQVWAEEF1 750	.:.:.: RCDGGEPELW 760	: .:::::::::::::::::::::::::::::::::	::::: TCLHSGAAQV 780	.::::::: /VCSVYTEVQI 790	:: :: MKNG 800
Hum.	910 920 930 940 950 960 970 KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGNESL	920 VLGHWGS	930 LCDTHWDP1	940 EDARVLCRQI	950 SCGTALSTIG	960 GKYIGERSVI	970 VVWGHRFHCLO	SNESL
WC1	TSQCEGQVEMKISGRWRALCASHWSLANANVVCRQLGCGVAISTPRGPHLVEGGDQISTAQFHCSGAESF 810 830 840 850	ISGRWRA:	.: ALCASHWSL/ 820	ANANVVCRQI 830	WRALCASHWSLANANVVCRQLGCGVAISTPRGPHLVEGGDQIS 820 830 840 850	GPHLVEGGDÇ 850	ISTAQFHCSC 860	3AESF 870
Hum.	980 LDNCQMTVLGAPPCI	990 PPCIHGN	1000 TVSVICTG	1010 SLTQPLFPCI	1000 1010 1020 1030 1040 HGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRC	1030 .VPEGSALICI	1040 EDKRLRLVDC	SDSRC
WC1	: .::.:: : LWSCPVTALGGPDCS 880	PDCSHGN'	::::::: NTASVICSGI 890	. :: : .: NHTQVLPQCN 900	::::::::::::::::::::::::::::::::::::::	ASEESSPYCS	SDSRQLRLVDC 930	: : 3GGPC 940
Hıım	1050 AGRVETYHDGF	1060 WGTTCDD	1070 SWDT.SDAH	1080 VVCOKTGCGV	1070 1080 1090 1100 1110 1110 CCDDGWDISDAHVVCOKIGGGVAFNATVSAHFGEGSGPIWIDDINCTGTESHIWOC	1100 1100	1110	COWIT
						· · · · · · · · · · · · · · · · · · ·) •• (• (•
M C.	GGKVEILDQGSWGTI 950	WGTTCDD.	ррмициияк 960	VVCKQLGCGE 970	CDDDWDLDDAKVVCRQLGCGEALNATGSAHFGAGSGFIWLDDLNCTGKESHVWRC 960 970 980 1010	GAGSGF1WL1 990	JOOO 1000	1010

Fig. 26N

1120 1130 1140 1150 1160 1170 1180 PSRGWGQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLG ::::::::::::::::::::::::::::::::::::	1190 1200 1210 1220 1230 1240 um. CGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDR ::::::::::::::::::::::::::::	1250 1260 1270 1280 1290 1300 -IRVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIW -:::::::::::::::::::::::::::::::::::	1310 1320 1330 1340 um. LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKSLNASSGHLALI :::::::::::::::::::::::::::::::::::
1160 1170 CAGRLEVFYNGTWGSVGRRN:::::::::::::::::::::::::::::::::::	CGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDR-:::::::::::::::::::::::::::::::::	1290 2QLGCGSALAA1 :::::::: 2QLGCGQALEA1 1200	1350 QSL :: TTAGTRTTSNSL 1270
0 ESCAGRLEVFYI ::::::: CAGWLEVFYI 1050	1230 WQCLSAPWERR:::::::::::::::::::::::::::::::::::	1280 SWDLAEAEVVC(::.::::: SWSLAEAEVVC(1190	RCSG :::: RCSGVRTTLPT
40 1150 TALRLYSETETE: : :	1210 1220 1230 GFMWVDDIQCPKTHISIWQCLSAPWERR :::::::::::::::::::::::::::::::::::	1270 HAGSWGTVCDD: :.::::::: HNGSWGTVCDD:	1310 1320 1330 1340 Hum. LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSG :::::::::::::::::::::::::::::::::
1130 1140 HKEDAGVICSEFTALRLYSE::::::::::::::::::::::::::::::::::::	1200 1210 LSKTGSGFMWVDDI . :: ::: GLREGSRPRWVDLI 0 1100	1260 DTECSGRVEIWI :.::::::: DSECSGRVEVWI 1170	1330 LWDCHAKPWGQ: :::: :::: LWDCVAEPWGQ: 1240
1120 1130 SRGWGQHDCRHKED::::::::::::::::::::::::::::::::::::	1190 13 CGENGVVSLAPLASTER 1000 1090	DRE:	1320 LDDMRCKGNESF: ::: :: LDEVQCGGRESS: 20 1230
Hum. Po	1 Hum. CG :: WC1 CG 1080	Hum WC1 CT	1310 Hum. LD] %C1 LD] 1220

Fig. 260

1410 SLEENLFHEME	:.::::::::	1440 DTSLLGV	. : .:: : .:: : .:: : .:: .:::: .::: .::: .::: .::: .:::::::::::::
1400 TRRRG	:: LIQKEGLGSF 1340	1430 DTPNHGCEDAS	:: GEGEESFWLLQ 1410
į	: SAVYEELDYI 1330	1430 DTPNHG	: :: NFSREAANPGEGEES 1400
1390 QKHLPLRVS	.: LSSYEDALAEA 1320	RTSD	:.:. RSSQTGSFLN 1390
1370 1380 LSSIFGLLLVLFILFLTWCRVQK	.: : LLRW-RAERRA 1310	1420 LKREDPHGTRTSD-	. : .:.:. EVPPEKEDGVRSSQ 1380
) 1380 LLLVLFILFL	:.: :.:	 	PSPSQGNEE 1370
1370 Hum. LSSIFGLI	: .: : WC1 LGSLLFI 1290	Hum. TC	WC1 EVPVPGT 1360

Fig. 261

1450 Hum. LPASEAT-K : .: .: WC1 LGTSPVTFS 1430

Hum. ATGATGCTGCCTCAAAACTCGTGGCATATTTGGAAGATGCTGCTGTCATCAGAACCTTTTCTCTG ::::::::::::::::::::::::::::	150 160 200 210 Hum. GTTGAGGCTGATCGAGGCTCCTGCTCTGGGACAGTGGAGGTGAAATTCCAGGGACAGTGGGGG :::::::::::::::::::::::::::::::	220 230 240 250 260 270 Hum. ACTGTGTGTGATGATGGAACACTACTGCCT-CAACTGTCGTGTGCAAACAGCTTGGATGTCCATTT ::::::::::::::::::::::::::::::::
---	---	---

Fig. 26Q-1

Fig. 26Q-2

Hum. WC1	560 5 um. ACTTGAATACTGCTG ::.:::::: WC1 TCACACTTGCCACTG 490 500	570 CTGCCGTGGTGT ::::: CTGCC	70 580 620 600 610 620 CGTGGTGTGCATCTTTTTTTTTTTTTTTGGAGTTGT ::::::::::::::::	590 AGGATGTCC?	600 ATCTTCTTTTA ::::::: ATCATCTGT	610 ATTTCTTCGGA GCAGAG	620 TTCTGGAGTTGT :::.:: -GCAGAGTTGGG 520
Hum. WC1	630 63 TAATAGCCCTGCTGT ::.: TTGTGGC		40 650 660 670 680 690 ATTGCGCCCCATTTGGCTGGATGACATTTTATGCCAGGGGAATGAGTTGGCACT:::::::::::::::::::::::::::::::::::	660 GATGACATT: ::::::	670 TATGCCAGGG :::::: CCTGGG	680 CCAGGGGAATGAGTT :::::::: CCTGGGACATGAG 50	690 GGCACT- :::
Hum. WC1	700 CTGGAATTGCAG :.:.: ::: CAGAGAGTCCAG 570	710 ACATCGTGGATG : T-GCC	710 720 730 740 750 760 TCGTGGATGGGGAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT : ::::: :::::::::::::::::::::::::::	730 CATGACTGCAGTCA :: :::: : CAGGTCTGGGC-	740 750 CACAATGAGGATGTCA ::::::::::::::::::::::::::::::::::::	750 ATGTCACATT ::: AGTTCA	760 AACTTGT : GG
Hum. WC1	770 TATGATAGTAG :.::: .: .: TGTGAGGGGGA	780 TGATCTTGAACTA :: ::::: GGAGCCTGAGCT- 620	780 790 810 820 830 CTTGAACTAAGGCTTGTAGGTGGAACTAACCGCTGTATGGGGAGAGTAGAGCTGA : :::.:: :: :: :: :: ::: ::: ::: ::: ::	800 STGGAACTAA ::::. GGGTCTGC	00 GGAACTAACCGCTGTATG :::: :: ::::: GGGTCTGCCC-CAGAGTG 640	820 :GGGAGAGTA ;;	830 GAGCTGA ::: -CCCTG- 650

Fig. 26Q-3

Fig. 26Q-4

Hum. WC1	1120 1130 Hum. AGCAGATGGAAGTAACAATTGTT .: .:::::: ::::::::::::::::::::::::::	1140 TGTTCAGGGAGAG ::::::: TGATCAGATCC 900	1150 TAGAGGTGA(::. :: TAACAGCCC(30 1140 1150 1160 11. AATTGTTCAGGGAGAGTAGAGGTGAGAATTCA-TGAACAGTCAGTCAGTCAGGGGAGAGTGAGAGTTTCACTGCTCTGGTGATCAG-ATCTAACAGCCCGATTTCACTGCTCTG900 910 920	130 1140 1150 1160 1170 1180 CAATTGTTCAGGGAGAGTAGAGAATTCA-TGAACAGTGGTGGACAATATG ::::::::::::::::::::::::::::::::	უ ტ () ტ
Hum. WC1	1190 TGACCAGAACTGGAA .:.::. ::: AGTCCT-TCCTGTGG 940	1210 ACAAGCCCTTG :::: CCT-G	210 1220 CCCTTGTGGTTTGTA ::: ::: : -CCT-GTGACT	1230 AGCAGCTAGGAT :: :::. -GCC-CTGGGTG 970	1200 1210 1220 1230 1240 1250 GAATGAACAAGCCTTGTGTTTGTAAGCAGCTTAGGATGTCCGTTCAGCGTCTTT:::::::::::::::::::::::::::::::	0 T: T.
Hum. WC1	1260 GGCAG-TCGTCGTGC ::::. :: : GGCAACACAGCCTCT 1000 10	1270 1280 1290 1300 AAACCTAGTAATGAAGCTAGAGACATTTGGATAAA: :: :: :: :: :: :: :: :: :: :: :: ::	1290 CTAGAGACA' : :: :: CCAGATCCA(1300 ITTGGATAAAC :: :: : GGTGCTTCCCC	1270 1280 1290 1300 1310 1320 TAAACCTAGTAATGAGACATTTGGATAAACAGCATATCTTGCACTGGG : :: :: :: :: :: :: :: :: :: :: :: ::	0 0
Hum.	1330 AATGAGTCAGCTCTC	1350 IGCACATATGA	1360 TGGAAAAGC	1370 AAAGCGAACATGCT	1340 1350 1360 1370 1380 1390 TGGGACTGCACATATGATGGAAAAGCAAAGCGAACATGCTTCCGAAGATCAGATG	06.5
WC1		 	255-	GGCCTCAGAGGACA-GCGCCC-	GCGCCCCCTACTG	. <u>r</u>

Fig. 26Q-5

1460 TATGG :: GCCGG	AATGC .:::: GATGC	TAAAG : CGGGG	TGTGA :: TGCCC
1400 1410 1420 1430 1440 1450 1460 Hum. CTGGAGTAATTTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGGGCTCATAGCCCCTGTTATGG :: ::::::::::::::::::::::::::::::	1470 1480 1490 1500 1510 1520 um. GAGATTGGAGGTGAAATACCAAGGAGAGGGGGACTGTGTGTCATGACAGATGGAGCACAAGG-AATGC ::::::::::::::::::::::::::::::::::::	1530 1540 1550 1560 1570 1580 1590 um. A-GCTGTTGTGTAAACAATTGGGATGTGGA-AAGCCTATGCATGTTTTGGTATGACCTATTTTAAAG :::::::::::::::::::::::::::::	1600 1610 1620 1630 1640 1650 1660 Hum. AAGCATCAGGACCTATTTGGATGACGTTTCTTGCATTGGAAATGAGTCAAATATCTGGGACTGTGA ::::::::::::::::::::::::::::::::::
1440 TGTCGGGGCTC? :.::::: -GACGGGG-GC-	1510 ATGACAGATGC :::::::: ATGACGGCTGC	1580 TGTGTTTGGT7 :: :: .: .: .::	1650 AATGAGTCAA/ :: :::: AAGGAGTCCC/
1430 ACCTAAGGCTT :::.::	1500 SACTGTGTGTC :: .::: CACCATCTGTG	1570 AAGCCTATGCATGT :::::	1620 1630 1640 1650 TTGGCTGGATGACGTTTCTTGCATTGGAAATGAGTCAAATATC ::::::::::::::::::::::::::::::
1420 AGGCAGATCTGGA ::::::: AGGCAGCTCCG0	1490 AGAGTGGGGG ::::: CTCCTGGGGG	1560 SATGTGGA-7 : ::::: :	1630 ATGACGTTT(: .:: : . ACAACTTGAA
1410 CTGATAAGGG :.: ::: CAGCAGGG	1480 ATACCAAGGZ . ::::::::::::::::::::::::::::::::::::	1550 1560 AAACAATTGGGATGTGGA-AAGCC::::::::::::::::::::::::::::::::::	1620 NTTTGGCTGG/ : ::: ::: NTCTGGTTGG/
1400 GTAATTTGTT	1470 SAGATTGGAGGTGAA :::: :::: .: .:	1540 GCTGTTGTGTGT7 :: :: :: :: : GC-GTGGTGTGC7	1610 AGCATCAGGACCTA :::::::::: AGGATCAGGGCCCA
Hum. CTGGAGT: WC1 CTCAGA-	Hum. GAGAT :::: WC1 GAGAG	1530 1540 Hum. A-GCTGTTGTGTGT7 :::::::: WC1 CCGC-GTGGTGTGC7 1230 1240	1600 Hum. AAGCA ::: WC1 CAGGA

Fig. 26Q-6

	T .	<i>(</i>) <i>1</i>	/h /h	(h
	1670 1730 Hum. ACACAGTGGGAAAGCATAATTGTGTACACAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA Hum. ACACAGTGGGAAAGCATAATTGTGTACACAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA : ::::::::::::::::::::::::::::::::::	.740 1750 1760 1770 1780 1790 1800 ACATGGGGCCTGGTGGCGCGCAGCAGCTGTACTTTCAAGGAC : :::::::::::::::::::::::::::::::::::	1810 1820 1830 1840 1850 1860 1870 Hum. GGTGGGCACAGTGATGACGGCTGGAACAGTAAAGCTGCAGCTGTGTGTAGCCAGCTGGACTG ::::::::::::::::::::::::::::::::::::	1880
(1/30 CAGGTG; ::: . CAGA(1800 .crrrc. ::.	1870 CAGCT(:::: CAGCT	1940 :GGCT(::::
7	CTCP	18 TGTACT : :::: TTTTCT	18 TAGCCA :: :: CAGACA	ATTT : : :CAGT
	CC T G	GGTG .:: AGTT 14	TGTA::::	30 AAAA . : GCCA
1	1/20 GTAA(::::	1790 TGGA(:::::	1860 GGTG' :.: GATC'	1930 ATGGAA :::: FTAGGC
•	1690 1700 1710 1730 1730 1730 1730 1730 173	AGACT TGGCT	crgr(: ccacc	GATAT(::::::::::::::::::::::::::::::::::
(116TC	0 GGGAF :::.	0 CAGC . :	1920 A-CAC : :: AGAAC
ן ר	1/10 AGGAT(:::: AGGAC(1410	1780 CTCGG(: : TGCTG(1850 GCTGC .::: ACTGT	1 TTCTA :::: TTAGA
	AGAG : AAGC	GCTGC: . :: AGTGT(TAAAG :. CATCA	CGCT:::CTCT
0	TACAC TACAC TEACAC GACAC	1770 CAACC : : :	1840 AACAG .: GAAGA	1910 GAAA : GTTG
•	STGT/	1 GCAGC : AGGAC	1 CTGGA : : : CATGG	1 FG-GG : : : FTCTG
_	ATTC:::	; : ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	: : : : : : : : : : : : : : : : : : :	GTC1
,	CATA/ CATA/ CACA/ CACA/ 1390	1760 TGGG(::::	1830 TGAC(:.::	1900 GCATGG(::.: CCTCAA(
	AAAG . :: GCAG	CTGG. ::: ATGG.	TGTGA':: TGCCG'	TGGC . : ACCC
0	80 80	1750 ccrGAGG ::: ::: ccrcAGG	.820 %AGTGT .:::	90 TCAT : TGGA
	1680 ACAGTGGATGGGGA : : : : ::::: CCGGGGCTGGGGG	1750 3CCTGA(:::: 3CCTCA(1820 CACAGT(:: .:: CAGTGT(880 1890 CCCATCTTCTATCATT
	CAGT(.::: GGCC	0 TGGGGCA(:::::: TGGGGCA(ATCT'
1	ACAC TTCC	1740 ACAI :- -CT-	1810 GGT(:	1880 CCC2 T(
,	fum. WC1	1 Hum. WC1	dum. WCl	Hum. WC1
		H	-	-

0 1610 **Fig. 26Q-7**

3AC .::	80 366 36A	50 AAT .:	20 3CA 3CA
2010 SAAATAATGAC ::::::::: GGAATTACAAC 1700	2080 CTTGTGGG :: ::::	2150 rgcraa' :: ::: rgarga	210 2220 AATCAGGGTCTCCA : ::: :::CCTGGACGCCA
GAAA : . : : GGAA	AGGC' : :C'	40 TCTGTG' : :: CATCTG' 1830	CAGGG: :: CCTGG
GG	2070 GAGCTG/ :: : GATCCG(2140 ATTC: :ACCA: 18:	2210 CAAT
2000 3GGTG- :.	ATGGA :: AGA	:GGGA ::: :GGGC	STCTG .: AGAAG
1950 1960 1970 1980 1990 2000 2010 ATGTTTCCTGTGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGGTGGGGAAATAATGAC ::::::::::::::::::::::::::::::::::::	2020 2030 2040 2050 2060 2070 2080 TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGGAGCTTGTGGG : :: ::: ::: ::: ::::::::::::::	2100 2110 2120 2130 2140 2150 TGCTGGAAAAGTTGAGGTGATGTCCAGGGTGCCGTGGGAATTCTGTGTGTG	2160 2170 2180 2190 2200 2210 2220 GGCTGGGGAATGAACATTGCTGTTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCA :::::::::::::::::::::::::::::::::
1990 'AGGAA(:: 'AGTGT(20 CATCG :: :: CAGCA	2.3	22 GAAT(: : : GGCT(
1 TGCA ::: GGCA	ATG-	20 GTCCA :.::: GACCA 1810	90 AACTT :.:: AGCTG 1880
30 3GTCA :CI	2050;TTCTG;::::;GTGTG(1740	2120 SAATGT .::. CCTTGA(2190 AGGCAA : . : : : . AAGCAG
1980 TCTCTGG' ::::: TCTCT	rcrgi :::: rcrgc	AGGTC::: AGATC	
AGATO : : ACCTO	2040 AGTG-A' : : : CCTATA' 1730	2110 GTTGAG :: ::: GTGGAG	2180 TTGTTT : :: : TGGTGT
1970 GAGATGAGTCA(::.:.::: GAAAACTGACA(1660	20 'GGAG .: AGCC	AAAA .:.: GAGA	GAAG : :CGTG
AGATG .:. AAAAC	ATGTT	2100 ;TGCTGG :::: ;CTCTGG	2170 ATTGCT ::: GATGCC
1960 GATGG/ :. ::: GTCGG/ 50	2030 SAAGA' .:::. AAAGG	21 GGTGTC : :: GCTGCJ	21 AACA1 .::.
19. TGTGA' .::: AGTGT(CAGT(:: CTCC/	90 AGCAG(.: : GGTCG(1780	60 GAATGAAC . :::: ACCTGGAC 1850
1950 196 IGTTTCCTGTGA1 .:::::: AGAATCCAGTGTC	2020 .AGTCA : :. .ATGCT	2090 TGGAAGCAGC :::::: TGGAGGTGGT	2160 GCTGGGGAA :::::: GCTGGGAC
1950 1960 1970 1980 2000 2000 2010 um. ATGTTTCCTGTGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGGTGGGGAAATAATGAC .:.::::::::::::::::::::::::::::::::::	202 TGCAGT : :: T-CATG	2090 um. TGGAAGCAGCAGGTG ::::::::::::::::::::::::::::::::::	
Hum. WC1	Hum. WC1	2090 2100 2110 2120 2130 2140 2150 Hum. TGGAAGCAGCAGGTGTGCTGGAAAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAAT ::::::::::::::::::::::::::::::::::	Hum. G WC1 C

Fig. 26Q-8

GA :: GA	AG .: GG	AA :: AA	CH :: H
2280 GGCTGCACTGGAGGGGA :::: .:::: AACTGCAGAGGAGGA	AGCA .::: IGCA 0	GTTG ::::	IG : ICAT
80 CTGG/ .:: GAGG/ 1970	2350 ATGGAA ::. GAAGAT 2040	2420 GACGT : . : GGCGA(2490 CAATG : : : CCAGG
2280 GCACT	23 AATA5 	24. TGGA.	24 :GCCA. ::: :GCCC.
GGCT.::AAACT	40 ATTTAA :: ATCATC 2030	GCTC	TGCI
2270 ATTCTG(:. AAGTGA)	2340 TCAT	2410 TGCCCT .:::: GACCCT	2480 TCTTCA: .:::
227 CGAATI .:. ATGAAG	0.676 0.16	rarg : rgga 20	rcrc .:.: acac 21
60 AATGT(. :: GCTGG;	330 -acrg :: cacaa)0 CTGA' .:: SAGA'	70 FITC
2260 CTTAA CTGGC	2330 2AG-AC	2400 GGAGCT :::: .	2470 CTGATT
CATCATC	saaac : scggc	367TC	SATTC :: SATGC
2250 2260 AGAACATTACACATCTTAATG' ::::: :::::::::::::::::::::::::::::::	2320 2330 2340 2350 TGGGAGTGGAAACAG-ACTGCGTGTCATTTAAATATGGAAGCAAG :::::::.::::::::::::::::::::::::::	2390 2400 2410 2420 CCAGGCTGGTTGGACTGATATGCCCTGCTCTGGACGTGTTGAA : ::::::::::::::::::::::::::::::::::	2450 2460 2470 2480 2490 ATGGCGCTCTGTCTGATTTCTCTCTTCATGCTGCCAATGT :::::::::::::::::::::::::::::::::
22 .ACAT	23 .GGGA .:::	233 CCAGGG: : : 2070	24();TGTCT();.::::::::::::::::::::::::::::::::::::
AAGA : .:: ACGGGA 1930	10 TACGAT : CTTCCT 2000	0 CAGC : C	0 GCTC : :
2240 ACAGAA- .:.:. ICGGGAC	2310 TATA	2380 CAGGC . :: TGTGC	2450 ATGGCG ::: CTGGAC 2130
2240 CACAGA .:.: ITCGGG	ATTG.	CCCA.	CACA
ATTT(:: CTTC' 1920	2300 ccrcrcrcrggga :: . ::: cccaagrarggag 80 1990	2370 CTCAGC ::::: CTCAGG	2440 GCAGA(::::::::::::::::::::::::::::::::::
2230 ccrca::::	2300 CTCTG : :: AGTATG	2370 ATCTGCTCAG :::::::: ATCTGCTCAG 0	24. ATGC::::
2 A-GC TCTC	CTCT	.60 TTGATC : ::: GTCATC 2050	AAAC :. ;catt
2230 2240 2250 2260 2270 2280 Hum. GAGA-GCCTCATTTCACAGAACATTTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGGA :::::::::::::::::::::::::::::	2290 2300 2310 2320 2330 2340 2350 Hum. AGCCTCTCTGGGATTGTATACGATGGGAGTGGAACAG-ACTGCGTGTCATTTAAATATGGAAGCAAG . :: . :: . :: . : :: . : :: . : : : :	23 F • 4	2430 2440 2450 2460 2470 2480 2490 Hum. GTGAAACATGCACATGGCGCTCTGTCTGTGATTTCTCTTCTTCATGCTGCCAATGTGCT ::::::::::::::::::::::::::::::::::::
Hum. WC1	2 Hum. WC1	Hum. WC1	Hum. WC1 21

Fig. 26Q-9

Hum. WC1	2500 2510 Hum. GTGCAGAGAATTAAA :::::::::::::::::::::::::::::::	2510 ATTAAATTGT ::::	2520 2530 TTGTGGAGATGCCATATCT(:::::::::::::::::::::::::::::::	2530 MTATCTCTTTC :::::::	2540 TGTGGGAGAT(:: : ::	2520 2540 2550 2560 TTGTGGAGATGCCATATCTCTTTCTGGGAGATCACTTTGGAAAAGGG-AATGG .:::: :::::::::::::::::::::::::::::::	2560 AGGG-AATGG :: .:::
2180	80	2190	2200	2210	2220	2230	2240
Hum.		2580 GGCCGAAAAG	2590 STTCCAGTGTG	2600 SAAGGGAGTG	2610 AACTCACCTT	2570 2580 2590 2600 2610 2620 2630 TCTAACTTGGGCCGAAAGTTCCAGTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAA	2630 CATTGTTCAA
WC1		::::: TGGGCTGAAGAG 2260	::: .:::: STTCAGGTGTG 2270	:.::::::::::::::::::::::::::::::::::::	:.::::::::::::::::::::::::::::::::::::	.: GGTCC 2300	TGCCCCAGAGTGCCC 2310
Hum.	2640 265 CATCCGGAAGACACT	2650 GACACTIGIA	2660 ATCCACAGCAG	2670 SAGAAGIIGG	2680 GTTGTCTGTT	0 2660 2670 2680 2690 2700 TGTATCCACAGCAGAGAGTTGGAGTTGTCTGTTCCCGATATACAGATGTCCGAC	2700 SATGTCCGAC
WC1	.:::.:::::: TGTCCAGGAGGCACA 2320 2330		::::::::::::::::::::::::::::::::::::::	:: .: : ;AGCTGCTCAC 2350	::::::::::::::::::::::::::::::::::::::	::: :::::: :::::::::::::::::::::::::::	::.:::::::::::::::::::::::::::::::::::
	2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATGGCAAAT	GCAAATCC	CAGTGTGAC	GGGCAAGTGC	AGATCAACGT	CCCAGTGTGACGGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGGCTCAC	IGGGGCTCAC
WC1	TT 23	ACGGCACCTC 2400	TCAATGTGAG 2410	GGGCAGGTGC 2420	SAGAT-GAAGA 2430	CCTCTCAATGTGAGGGCAGGTGGAGAT-GAAGATCTCTGGACGATGAGAGCGC	TGGAGAGCGC 2450

Fig. 26Q-10

COVEDIO CITUEL

Hum. WC1	2780 TGTGTGACACCCACT ::::::::::: TCTGTGCCTCCCACT	2790 GGACCCAGAA : : .: GAGTCTGGCC	2800 GATGCCCGTG :::::::::	2810 TTCTATGCA::::::	2790 2830 2810 2820 2830 GGGACCCAGAAGATGTTCTATGCAGACAGCTCAGCTGTGGGACT	2830 2840 CTGTGGGACTGCTCT ::::::::::::::::::::::::::::::::
Hum.		2480 2860 AAATATATTG	2490 2870 GAGAAAGAAG	2880 STGTTCGTGTC	2890 GTGGGGACAC	2860 2870 2500 2520 2520 2520 2520 2520 2860 2870 2880 2890 2900 2910 2910 2910 2910 2910 2910 29
WC1	CTCCACCCCCAGAGGA 2530 2540 2920	.ccacactTgg 2550 2930	;TGGAAGGAGG 2560 2940	FIGATCAGATC 2570 2950	CTCAACAGCCC 2580 2960	CAATTTCACTGCTCA 2590 2970 2980
Hum.	CACTT	TGGATAACTG	TCAAATGAC <i>F</i>	GTTCTTGGA:	GCACCTCCCT(CTGGATAACTGTCAAATGACAGTTCTTGGAGCACCTCCCTGTATCCATGGAAATA
WC1	GGGGCTGAGTCCTTCCTGTGAGTTGTCCTGTGCCTTGGGTGGG	rgrggagtrg 2620	TCCTGTGACT 2630	GCCTTGGGT(2640	GGCCTGACT(2650	GTTCCCATGGCAACA 2660
Hum.	2990 CTGTCTCTGTGATCTG	3000 CACAGGAAGC	3010 CTGACCCAGO	3020 CACTGTTTC	3030 CATGCCTCGC	3040 3050 AAATGTATCTGACCC
WC1	::::::::::::::::::::::::::::::::::::::	::::::: CTCAGGAAAC 2690	::::::::::::::::::::::::::::::::::::::	::: : ;TGCTGCCCZ	.::: .:: AGTGCAACGA(2720	: .::: .: :: :: :: :: :: :: :: :: :: ::

Fig. 26Q-11

Hum. WC1	3060 3070 3080 3090 3100 ATATITGICIGCAGTICCAGAGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGC	3110 3120 :rccgccragrggar :::::::::::::::::::::::::::::::
Hum. WC1	3130 3140 3150 3160 3170 GGGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCAC ::::::::::::::::::::::::::::::::	3180 3190 CATCTGTGATGACG :::::::::::::::::::::::::::::::::::
Hum. WC1	3200 3240 GCTGGGACCTGAGCGATGCCCACGTGTGTGTCAAAAGCTGGGCTGTGGAGTGGCC .::::::::::::::::::::::::::::::::::	3250 3260 TTCAATGCCACGGT ::::::::: CTCAATGCCACGGG
Hum.	3270 3310 3280 3290 3300 3310 3310 CTCTGCTCACTTTGGGGGGGGGCCCATCTGGCTGGATGACCTGAACTGCA.::::::::::::::::::::::::::::::::::::	3320 3330 CAGGAACGGAGTCC :::::::::::
) A		3010

Fig. 26Q-12

Hum. WC1	CACTTG ::: :: CACGTG 3020	3340 CACTTGTGGCAGTGC :::::::::::::::::::::::::::::::::::	3350 CCTTCCGCGG:::::::::::::::::::::::::::::	3360 GGCTGGGGGCA ::::::::: GGCTGGGGGCG	3370 AGCACGACT .:::::: GGCACGACT	3380 CTGCAGGCACAAGG :::::::::::: CTGCAGACACAAGG	3340 3350 3400 3400 3400 3400 3400 3400	3400 GGTCA ::::: GGTCA
Hum. WC1		3410 TCTGCTCAGAATTCA :::::::::: TCTGCTCAGAGTTCC' 3090 3100	3420 34 CAGCCTTGAGGCT .::::::::	3430 GGCTCTACAG :: : : : GGATGG	3440 TGAAACTGA ::::::: TGAG-CGAG	3450 AACAGAGAGCT ::: :::: GACCAGCAG-T 3130	3420 3430 3440 3450 3460 3470 CAGCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGTTTGGA .:::::::::::::::::::::::::::::::::::	3470 ITGGA :::: CTGGA
Hum. WC1	m. AGTCTT .::::	3480 AGTCTTCTATAACGG :::::::::::	3490 GACCTGGGGG ::::::::	3500 CAGCGTCGGC ::: :: :: CAGTGTCTGC	3510 AGGAGGAAC : :: : CGCAGCCC	3520 ATCACCACAGC :: ATGGAAGATAT	3480 3490 3500 3510 3520 3530 3540 um. AGTCTTCTATAACGGGACCTGGGGCAGCGTCGCCAGGAACATCACCACACCCATAGCAGGCATTGTG ::::::::::::::::::::::::::::::::	3540 TTGTG : .: TGATC

Fig. 26Q-13

oczeczen czeczenie

Fig. 260-14

						3750	3760
Hum.		DDL				-GTGGAGGAG	-GTGGAGGACACCGAGTGCTCTG
						••	
WC1	TGTCCAP	WC1 TGTCCAACTGCTGCCG	CCTGCACAGA	CAGAGAGAAG	CICCECCIC	AGGGGAGGAG	CCTGCACAGACAGAGAAGCTCCGCCTCAGGGGAGGAGACAGCGAGTGCTCAG
	3430	3440	3450	3460	3470	3480	3490
7.5	9770	3780	3790	3800	3810	2820	3830
Hum.	GGAGAGI	GGAGATCTG	GCACGCAGGC	TCCTGGGGCA	CAGTGTGTG	ATGACTCCTG	Hum. GGAGAGTGGAGATCTGGCACGCAGGCTCCTGGGGCACAGTGTGATGACTCCTGGGACCTGGCCGAGGC
					•••	•••	
WC1	6666661	rggaggrgrg	GCACAACGGC	TCCTGGGGCA	CCGTGTGCG	ATGACTCCTG	WC1 GGCGGGTGGAGGTGTGGCACAACGGCTCCTGGGGCACCGTGTGCGATGACTCCTGGAGCCTGGCAGAGGC
	3500	3510	3520	3530	3540	3550	3560
			٠				
38	3840	3850	3860	3870	3880	3890	3900
Hum.	GGAAGTG	GTGTGTCAG	CAGCTGGGCT	GIGGCICIGC	TCTGGCTGC	CCTGAGGGAC	Hum. GGAAGIGGIGICICAGCAGCIGGGCIGIGGCICIGCICI
	•••				•••••		
WC1	TGAGGTG	SGTGTGTCAG	CAGCTGGGCT	GTGGCCAGGC	CCTGGAAGC	CGTGCGGTCT	WC1 TGAGGTGTGTGTCAGCAGCTGGGCTGTGGCCAGGCCCTGGAAGCCGTGCGGTCTGCAGCATTTGGCCCT
	3570	3580	3590	3600	3610	3610 3620	3630

Fig. 26Q-15

	35 Hum. 35 Hum. WC1	3920 GGAACCATCT :::::::::::::::::::::::::::::::::::	3930 rGGTTGGATG2 ::::::::::::::::::::::::::::::::::::	3940 ACATGCGGTGG : : . : : : 3670 4010 FGGACACAAGG : : : : : : : : 3740 3740 . : : . : : : : : : : : : : : : : : : :	3950 CAAAGGAAATG CGGGGGCCGGG 3680 SAAGATGCTGG SAGGATGCTGG 3750 1070 CCTCAGGT-CA CCTCAAATTCT 3820	3960 ::::::::::::::::::::::::::::::::::::
Hum Hum Hum Hum Hum Hum			3920 GGAACCATCT :::::::::::::::::::::::::::::::::::	3920 3930 GGAACCATCTGGTTGGATG2 ::::::::::::::::::::::::::::::::::::	3920 3930 3940 GGAACCATCTGGTTGGATGACATGCGGTGC :::::::::::::::::::::::::::::::	3920 3930 3940 3950 GGAACCATCTGGTTGGATGACATGCGGTGCAAAGGAAATG ::::::::::::::::::::::::::::
3950 396 GGTGCAAAGGAAATGAGTC ::::::::::::::::::::::::::::::::::::	3920 3930 3940 3950 3960 3960 3960 3960 3960 3960 3960 3960 3960 3960 3960 3960 3960 3960 3690 3640 3650 3660 3670 3680 3690 3640 3650 3660 3670 3680 3690 3690 3690 3690 3690 3690 3690 3690 3690 3690 3690 3690 3750 3760 3770	3930 3940 3950 3960 IGGTTGGATGACATGCGGTGCAAAGGAAATGAGTCATTTCT ::::::::::::::::::::::::::::::	3940 3950 3960 ACATGCGGTGCAAAGGAAATGAGTCATTTCT .::::::::::::::::::::::::::::::::	3950 3960 CAAAGGAAATGAGTCATTTCT CGGGGCCGGGAGTCCTCCCT 3680 3690 3680 4030 SAAGATGCTGGCGTGAGGTGC SAGGATGCTGCTGTGAGGTGC 3750 3760 4070 4080 CCTCAGGT-CATTTAGCF CCTCAAATTCTCTCCCTGGCF 3820 3830	3960 ::::::::::::::::::::::::::::::::::::	

Fig. 26Q-16

Hum. WC1	Hum. G : WC1 GGGGTT 3850	4100 TATCTT : ::: CTCTGCCTT	4110 TGGGCTC-CTT ::::::::::::::::::::::::::::::::	-CTTCTC ::::: GCTTCTCTTC 3880	4110 TGGGCTC-CTTCTCCTGGTTCT ::::::::::::::::::::::::::::::::::	4110 4120 4130 4140 um. GTATCTTTGGGCTC-CTTCTCCTGGTTCTGTTTATTCTATTTCTCA : :::::::::::::::::::::::::::::::::::
Hum. WC1	41 CGTGGTG .:::.: GATGGAGAG 3920	4150 'GCCGAGT : ::: 'GAGCAGAGC	4150 4160 4170 CGTGGTGCCGAGTTCAGAAACAAAACATCT::.: :::::::::::::::::::::::::::::::	4170 AACATCT :::: CCAGCTATG 3950	GCCC ::: SAAGATGCTCTT	4150 4160 4170 um. CGTGGTGCCGAGTTCAGAAACAACATCTGCCCCTCAGAGTTT::::::::::::::::::::::::::::::
Hum. WC1	 CGATTA 3990	4190 CAAC :: ACCTTCTGAC 4000	4210CAGAAGGAGGGTTCT-CTCG- ::::::::::::::::::::::::::::::::::::	5GTTCT- : : :. STCTGGGCAG	4210 CT-CTCGAGG :. : . :: CAGCCCAGATCAGA 0 4030	4190 4200 4210 4220 umCAACCGTTCT-CTCGAGGAGAATTTATTCCATGA :: :::::::::::::::::::::::::::::

Fig. 26Q-17

υ	ن ن	ı O	₽ ₽
4250 AAGAGAGAGGAC :-::::::::	WC1 TATGATGATGCTGAAGTACCAGTGCCTGGAACTCCTTCTCCCTCTCAGGGGAATGAGGAAGTGC 4060 4070 4080 4090 4100 4110 4120	4260 4270 um. CCACATGGGACAAGAACCTCAGA-TGACACCCCCAA :::::::::::::::	430 430 umCCATGGTTGTGAAGATGCTAGCGACAC
	4110	 SAACTT(4320 ATCC GGGGATC
U	rctc2	00	,
-DEDD	TTCTCCC 4100	GACAC	 .AGGGGAA(
4240 -ACCTG	CCTGGAACTCC 4090	4280 CTCAGA-TGACACCC ::::::::::::::::::::::::::::	1130 0 CTAGCGACAC-:::::: CTGGCTGCTCC
42 A	AGTACCAGTG 4080	GGGTGAGGT(4310 AAGATGCT :::: ::: AAGAGAGCTTCT
:	ATGCTGAAGA 4070	4260 4270 Hum. CCACATGGGACAAGAAC- ::::::::::: WC1 CCCCAGAGAAGGAGGACG	4310 4310 CCATGGTTGTGAAGATGCTAGCGACAC- ::.::::::::::::::::::::::::::::::::::
4230 GATGGAG	TATGATG 4060	4260 CCACATG :: :: . CCCCAGA	CCA CCA TAATCCT 4200
Hum.	WC1	Hum. WC1	Hum. WC1

Fig. 26Q-18

Fig. 26Q-19

32 127 12 67 52 187 72 247 92 112 132 152 487 367 S AGC G GGG A GCA D GAT E GAA T ACC GGA GGA PCCA V GTT A GCG R AGG L E GAG G GGT D GAT S AGT $^{\rm C}_{
m TGT}$ Q CAG K AAG M ATG CCC R CGT S AGT A GCT L I ATC K AAA T ACG E GAA R CGT PCCT K AAG TACG R AGA I ATC D GAT L D GAT S AGC G GGC P G GGG L CTG L TTG D GAC $^{\mathrm{F}}$ F TTC D GAC E GAG A GCA A GCC N AAC A GCC L T ACT S AGT S TCG L Y TAT D GAC $_{
m L}$ A GCC FTTC FITC I ATC L Y TAC I ATT P CCA TACC FTTT CCCC Q CAG R AGA D GAT A GCC W TGG Q CAG GGC PCCG $_{
m L}$ GCC Q CAG T ACA C GIC E GAA L CTT \gt ATG R AGG L I ATA E GAG T ACC L CTG L R CGA Q CAA GGC M ATG N AAT $^{
m Y}$ $^{
m Y}$ GICGACCCACGCGICCGGICTGIGGCTGAGC P CCC A GCT S TCC FTC M ATG K AAG G GGG N AAC S AGC L V GTG K AAG K AAG D GAT L CIC PCCC Q CAG H CAT TIC H CAC Y FAC L CTA K AAG TACC Q CAA G GGG LCIT Q CAG FTTC L R AGG K AAG V GTC LCTT 9 96C GGG F TTC TACT PCCC FTTT N AAT E GAA Y TAC I ATT $_{\rm L}$ N AAT A GCC 9 9 9 9 S AGC V GTC GGG $_{
m TTC}$ LCIT GGA S TCT L GGA CTGT

Fig. 27A

352 1087 252 787 232 727 292 907 D GAC LCTC S TCC S AGC A GCC . GGG G GGG A GCC N AAT P 9 R CGC D GAC T ACA K AAG Q CAG E GAG H CAT CA GCC Q CAG E GAG K AAG W TGG H CAT R CGT $_{
m L}$ L F TTC R AGA A GCG Q CAG E GAA PCCC W TGG FTTC A GCT FTTC H CAC S TCC E GAG T ACC T ACC D GAC R CGC $^{
m F}$ R CGC YTAC R CGG T ACC I ATC $_{
m L}$ S AGT F TTC 9 96C FTTC S TCG W TGG V GTC K AAG N AAC TACA A GCA S TCT F ITC D GAC Q CAG H CAC K AAG FTTC Y TAC FTTC TACC T ACC Q CAG A GCC P N AAC L CTC P I ATC N AAC K AAG S TCG R AGG L CTG $_{
m L}$ H CAC CTGT M ATG L EGAG L CTG Q CAG PCCT PCCC PCCC TACT K AAG A GCG V GTC I ATC FTTT G GGG A GCT S AGC A GCC FTTC E GAA P T ACA S TCT GGT PCCT S ICT Q CAG A GCA D GAC GGC Q CAG PCCC S AGC R AGG S TCC F TTT GGC T ACC S TCT GGA E GAG V GTG F TTT C TGC D GAT

Fig. 27B

452 1387 392 432 9 9 S AGC L CTG L CTT CCC D GAC N AAC S TCT H CAT R AGG K AAA S AGC G GGG R \overline{W} R CGG N AAC PCCT H CAC S AGT P CCC R AGG L CTG G GGG A GCC A GCC P CCT GGT D GAT E GAA G GGA S TCT D GAT PCCC L S TCA A GCT PCCT CTGT T ACG K AAG G GGC D GAC FTTC D GAC S TCT GGG Q CAG H CAC W TGG S TCC PCCT GGC C TGC P V GTG A GCC L FTTC $_{
m TGT}$ R $^{\rm C}_{
m TGT}$ T ACC 9 9 T ACA S TCG L S AGC F TTT Q CAA E GAG GGG Q CAG E GAG R CGA GAA E GAG A GCA S TCA V GTG T ACA S TCC Y TAT 되 TACC E GAG E GAG C TGC D GAT A GCA GGT M ATG TACC E GAA Q CAG S AGT LCTT S AGT PCCT GGC $_{\rm CTG}$ R CGG GGA V GTG TACC D GAC $^{\rm C}_{
m IGT}$ E GAG F TTC T ACA $_{
m L}$ $_{
m CTG}$ P N AAC W TGG P CCA H Y TAT Y TAC H CAT A GCC A GCC A GCC R CGG E GAG M ATG Y TAC P D GAC A GCT L R CGA $^{\rm C}$ K AAG V GTG V GTC Q CAG H CAC N AAC S AGT PCCC

Fig. 27(

652 1987 552 687 592 807 612 867 632 927 PCCC L CTG S AGT S TCA E GAA A GCC A GCC A GCT P CCC W TGG $_{
m ITG}$ FTT G GGG R PCCT FTTT 9 A GCT Y TAT L CTC 9 9 9 9 D GAT GGT LCIC LCTC L S TCC A GCA S AGT Y TAT N AAT LCTG S AGT V GTC A GCC V GTC GGC E GAG A GCC V GTC R AGA S TCT T ACT E GAA A GCC N AAT T ACT L R AGG V GTC $\frac{L}{\Gamma\Gamma G}$ CTGT A GCA K AAA L TTG Y TAC A GCA TACC TACC T ACT PCCA A GCC Q CAG S TCC W TGG I ATT V GTC W TGG L ITG V GTC E GAG I ATC S TCA TACT C FGC D GAC P A GCC FTTTV GTG P CCA Q CAA L S TCC Q CAG Q CAG V GTC H CAC L CIC PCCG Y TAC K AAG P CCC N AAC H CAC S TCT S AGC GGG A GCC L D GAC V GTG W TGG R P I ATC V GTG IATC R E GAA Y TAC S AGC C TGC GGT H CAT E GAG Q CAG PCCC P CCA GGG W TGG EGAG S LCTC ATG Y TAC R CGG Q CAG A GCC PCCT LCIC V GTC V GTT Σ D GAC E GAG A GCA GGA S TCC Q CAG GGA P R Q CAG A GCA D GAT I ATC S TCA CTT L IATC A GCC Q CAG K AAG S AGC I ATC PCCA V GTG 3 3 6 6 6 7 A GCT L CTT W TGG A GCA V GTG R AGG S TCC 9 V GTG PCCT Γ I ATA L TTA S TCC S AGC N AAC H Y TAC LCTG A GCC

Fig. 27D

TOPEDIOL OTTOPOL

732	GAG ACC CTG CGC CCT GGG GAG AAG GCC CCG TTA AGC AGA 2227	752	AAG GAA TGC AGG ACC TCT GCC AGT GAT GTG GAC GCT GAC 2287	762	2317	ACTCTAGGCACAGGCCGGGGGTGCAGGCACCTGGCCATGCTGGCTG	TGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGG 2475	TGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCC 2554	CCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAA 2633	CACAGTGTTTCAAGAGATCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCCAAACATCTAAACAATC 2712	ATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCA 2791	TGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACC 2870	ACCTITCTICTICTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT 2949
ፈ	AGA	Ω	GAC			AGGA	4GGG	ACCC	3AAA	AATC	STCA	3ACC	LTCT
ഗ	AGC	A	GCT			SACTA	CAGC	3GCT	rcca(AAAC1	CAGG	STCT(4GCC.
Н	TTA	Ω	GAC			CCT	CACT	rggg(ACCC	ATCT/	CICC	rgaa(rcr <i>g</i> i
ሲ	SCG	>	GTG			4CAG	4TGA(4GGG.	4GGG/	AAAC!	CCTT	LTCC.	3TAA
A	SCC	Ω	GAT			AAGC?	4CTG2	PAAC?	LTCC	CACCA	ACTC	STCT	4GGG(
X	AAG	ഗ	AGT			3CCC7	CATCA	CTC	3CCA1	rgaa(CAAC	3GAA(rggc7
囝	GAG	Ą	CCC			3666	rctg	3AGC.	rcrg(3TAA.	ACAC	CCCAC	4GAA.
ტ	GGG	ഗ	TCT			SCTG	CTAC	ACATO	CAGT	ratg(rrgg/	3ACT(rggc7
ρц	CCI	⊢	ACC			SCTG	rctg(AAGC7	CCTT	ACCC	GCT	CGCT(3000
ፈ	၁၅၁	ĸ	AGG			CCAT	AGCT.	racc?	3GAT(ZAGG/	CIGC	3CAC(LTCT(
Ц	CIG	ن ت	TGC	*	TAA	CTGG	3AGG	CTTC	3AGA(3TCC(3AAG	rcgT(ICCC
H	ACC	ഥ	GAA	Ą	G GTA GCT TAA	SCAC	CTGA	CICCO	CTG	SCCT	CICIO	CAG	CTGA
田	GAG	凶	AAG	>	GTA	SCAGO	וכככנ	3GGA(4GAA(ACCT(rcca(CTTA(3ACT(
ပ	IGI	д	CCC	ഥ	GAG	GGT	[TTC]	CTAT	rTGA2	AAAA	LAAAC	LTCC	3GCA(
ტ	299	တ	TCT	₽	ACT	3CTG(CACC	rccc	SATA	CTAA	CTGG	CIGC	rTGG
Ø	CAG	Ø	CAG	Ŋ	GGC	3666	4GAC(rgcc.	CACT	3ATC(ACTC	CCTC	rcag.
>	GTT	П	CIC	Ц	CTA	4GGC(CAAAI	AGTC	CCTA	4AGA(rgcc1	3CIC(rgcT.
×	AAG	Ħ	CAC	ပ	TGC	3CAC	4GCA(CAGC	IGCT(LTTC	AACA	ATCT(FTCT
ტ	CGG GGC AAG GTT CAG GGC	E Q H L Q S P	GAG CAA CAC CTC CAG TCT CCC	N N C L G T E	AAC AAC TGC CTA GGC ACT GAG	CTAG	CAGC	rgca(3ACC.	4GTG.	rgc _T ;	4GGG	TTTC.
~	990	떠	GAG	Z	AAC	ACT	TGA(TGA.	CCA	CAC	ATA.	TGC	ACC.

Fig. 271

TCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCTTTTTCCTTTTGGGATTCAGAAAACTGCTTGTC 3028

Fig. 27F

Hum. Mur. Mur.	290 KKWTTFLKAQLLCTQ ::::::::::::::::::::::::::::::::::::	300 PGQLPFNVIRH ::::::::::: PGQLPFNVIRH 300 370 TYRGPETNPRP ::::::::::: TYRGSEVSPRP 370 440 LGTTTGSLHKA	310 AVLLPADSPT:::::: AVLLPADSPS: 310 380 GSCSVGPSSD: GSCSMGPSSD: 380 450 VVSGDSSAHL	320 APHIYAVFTS(::::::::::::::::::::::::::::::::::	330 SWQVGGTRSSP SWQVGGTRSSP 330 400 MDEQVVGTPI MDEHVVGTPI 400 470 EPVRNLQLAPT	300 310 320 330 340 350 PGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF :::::::::::::::::::::::::::::::::::
Mur.		::::::::::::::::::::::::::::::::::::::	.:.:::::::::::::::::::::::::::::::::::	.:::::::::::::::::::::::::::::::::::::	EPVRNLQLAPA	PDSEPVRNLQLAPAQGAVFAGFSGGIW 470 480
Hum.	500 RVPRANCSVYESCV	510 CVLARDPHCAW	520 DPESRTCCLL	530 SAPNLNSWKQI	540 OMERGNPEWAC	510 520 530 540 550 560 DCVLARDPHCAWDPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRPQS
Mur.	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	::::: ::: DPESRLCSLL, 520	:::: SGST-KPWKQI 530	::::::::::::::::::::::::::::::::::::::	TRGPMARSPRRQS 550

Fig. 27G

630	WATENG	•••	VATENG		700	LSGALI	:	LLGVLT						
620	LELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG		LELRCPHLSALASYHWSHGRAKISEASATVYNGSLLLLPQDGVGGLYQCVATENG	620	069	FVTVTVLFALV		FLIVTVLLAIV	069	760	NCLGTEVA	•••	NHLGAEVA	760
610	TVYNGSLLLI	•	TVYNGSLLLL	610	089	LAAQQSYWPH	••••••	MAAQRSYWPHI	089	750	TSASDVDADNN		TSASDVDADNN	750
009	PAAVPEASS	:	RAKISEASA	009	670	LTRVSGGAA	•	LTRVGGGAS	0.29	740	HLQSPKECR		HLQPSKDHR	740
590	ALASYYWSHG		ALASYHWSHG	290	099	GIPREHVKVF		GVPRERVQVE	099	730	GEKAPLSREÇ	••	REKAPLSRDÇ	730
580	LELPCPHLS		LELRCPHLS	580	650	2TLALDPELA		PLALDPELA	650	720	KVQGCETLRP	••	KVQGCGMLPP	720
570	Hum. RPQIIKEVLAVPNSI		Mur. PPQLIKEVLTVPNSI	570	640	Hum. FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALI		Mur. YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVLT	640	710	Hum. ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA		Mur. LLLASPLGALRARGKVQGCGMLPPREKAPLSRDQHLQPSKDHRTSASDVDADNNHLGAEVA	710
	Hum. R.		Mur. P.	260		Hum. F	•	Mur. Y	630		Hum. I	•	Mur. L	700

Fig. 27H

Fig. 271

310 GGGGTCCC :::: GGAATCCC	380 AGAAGAAG :::::: AGAAGAAG	450 CTACACCT ::: .:: CTATGCCT	520 CCCATCTC ::::::
290 310 CTGGCCTTGGATATCCAGGATCCAGGGGTCCC::::::::::	GCCTTTAL ::::::: FGCCTTTAL	ACCCATCT(:: :: :: ACTCACCT(480	ACCTGTTGC .::::::
300 SGATATCCA : .:::::: SAATATCCA 330	370 AGTGAATGT : ::::: ACCGAATGT(440 ACAATGTCA(::::: :: ACAATGCTA(470	510 AGATTCCTA ::::::.
290 CTGGCCTTC :::::::: CTGGCCTTC 320	360 GAAAAAAG <i>I</i> ::::::::: GAAAAAAG <i>I</i> 390	430 GGTTTCTT <i>F</i> :::::::: GGTCTCTT <i>F</i> 460	500 GAACTTCA? :::::: GAACTCCA? 530
F 1 7 3	350 AGTGACA ::::::	420 STGTCCT :.::::	490 CTTCATT :::::
270 280 GTGGGGCTCGAGAAGCCATJ ::::::::::::::::::::::::::::::::::::	340 TGGCCAGCC :::::::: TGGCCAGCC	410 ACTTCATCC(::::::: ACTTCATTC(480 TGCTTGTAC ::: :::: TGCCTGTAC
2 ACGTGGGG : ::::: ATGTGGGG	370	4 TGTTTCAP :::::::::: TGTTTCAP	'TCAGCCCT'::::::::::::::::::::::::::::::::::
260 TACTCTCTP::: CACTCTCTP	320 330 AGGCTAAAGAACAT(::::::::::::::::::::::::::::::::::	390 400 AGCAATGAGACACAG ::::::::::: AGCAATGAGACACAG	470 CCTTCGCCTT :::::::::
250 1. ATGGAAAT 2::::: 280	2	390 AGCAATG :::::: . AGCAATG	460 GCGCCCCTTC : ::::: . GTGGGACCTTT 490 500
Hum. Mur. 28	Hum. Mur.	Hum. Mur.	Hum. Mur.

Fig. 27J

Fig. 27K

COFFER OF CHINE

Fig. 27I

1090 1100 1110 1120 1130 1140 1150 GGGAAATACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCC :::::::::::::::::::::::::::	1160 1170 1180 1190 1200 1210 1220 GGCCAGGCAGTTGCTCAGTGGGCCCTCTGATAAGGCCCTTCATGAAGGACCATTTCCTGAT :::::::::::::::::::::::::::::::::::	1230 1240 1250 1260 1270 1280 1290 Hum. GGATGAGCAAGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAG ::::::::::::::::::::::::::::::::	1300 1310 1320 1330 1340 1350 1360 ACAGCCCAGGGCCACCAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACA .:::::::::::::::::::::::::::::::::
1090 110 Hum. GGGAAATACAAAGAG :::::::::::::::::::::::::::::::	1160 Hum. GGCCAGGCA :::::::: Mur. GGCCAGGCA	1230 124 Hum. GGATGAGCAAGTGGT :::::::::::::::::::::::::::::::::	1300 Hum. ACAGCCCAG .:::::::: Mur. TCAGCTCGG

Fig. 27M

1370 1480 1410 1420 1430 AGGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACC ::::::::::::::::::::::::::::::::::::	1440 1460 1470 1480 1500 TGTTCGCAACCTGCTGCTTTTGTAGGCTTCTCAGGAGGTGTCTGGAGG :::::::::::::::::::::::::::::::::::	1510 1520 1530 1540 1550 1560 1570 GTGCCCCGAGCCAACTGTTATGAGAGCTGTGTGGACTCTTGCCCGGGACCCCCACTGTG ::::::::::::::::::::::::::::::::::	1580 1590 1600 1610 1620 1630 1640 CCTGGGACCCTGAGCTCCTGGAAGCAGGACAT	::::::::::::::::::::::::::::::::::::::
1370 Hum. AGGCTGTGGTA :::::::::: Mur. AGGCTGTGGTG 1400 141	1440 Hum. TGTTCGCAAC :::::::::: Mur. TGTTCGAAAC 1470	1510 152 Hum. GTGCCCGAGCCAAC :::::::: Mur. GTTCCCAGGGCCAAT 1540 1550	1580 Hum. CCTGGGACCC	::::::: Mur. CCTGGGACCC 1610 16

Fig. 27N

Hum.		1660 SAACCCAGAGT	1650 1660 1670 1680 1690 1700 1710 GGAGCGGGGGAACCCAGAGGCATGTGCCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGC	1680 MGTGGCCCCA	1690 TGAGCAGGAG::::::	1700 GCCTTCGGCCT	1710 CAGAGCCGC ::::::::
Mur.		CAACCCGGAGT 1690	GGAACGCGGCAACCCGGAGTGGGTATGCACCCGTGGCCCAGGAGCCCCCGGCGTCAGAGCCCC 1680 1690 1700 1710 1720 1730 1740	CGTGGCCCCA 1710	TGGCCAGGAG 1720	1730	CAGAGCCCC 1740
Hum.	1720 CCGCAAATCA	1730 ATTAAAGAAGT	1720 1730 1740 1750 1760 1770 1780 CGCCAAATCATTAAAGAAGTCCTGGCTCCCCAACTCCATCTGGAGCTCCCTGCCCCCCCC	1750 CCAACTCCAT	1760 CCTGGAGCTC	1770 CCCTGCCCCC	1780 ACCIGTCAG
Mur.	:: ::: ::::: CCTCAACTAATTAAA 1750 1760	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	::::::: CCTGGAGCTG 1790	: :::::: GGCTGCCCCC 1800	::::::: ACCTGTCAG 1810
	1790	1800	1810	1820	1830	1840	1850
Hum.		STTATTATTGG	CCTTGGCCTCTTATTAGGAGTCATGGCCCCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGG	CAGCAGCAGTC	CCAGAAGCCI	CTTCCACTGT	CTACAATGG
Mur.	: ::::::: CACTGGCCTCTTA	::: : ::: TTACCACTGG	: ::::::::::::::::::::::::::::::::::::	SAGCCAAAATC	TCAGAAGCCI	:: :: :: :: :: :: :: :: :: :: :: :: ::	::::::: CTACAATGG
	1820	1830	1840	1850	1860	1870	1880
	1860	1870	1880	1890	1900	1910	1920
Hum.		SCTGATAGTGC	CTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTT	IGGGGGTCTCT	ACCAGIGCIG	GGCAACTGAG	AATGGCTTT
				••••••	•••		
Mur.		SCIGCIGCCGC	CTCCCTCTTGCTGCTGCCGCAGGATGGTGTCGGGGGCCTCTACCAGTGTGTGGGGGCGACTGAGAACGGCTAC	GGGGCCTCT	ACCAGTGTGT	GGCGACTGAG	AACGGCTAC
	1890	1900	1910	1920	1930	1940	1950

Fig. 270

Hum.	_	1940 TGATCTCCTAC		1960 GCCAGGACCA	1970 GACCCTGGCC	1980 CTGGATCCTG	1990 AACTGGCAG
Mur.	TCATACCCTGTGGTC	 TGGTCTCCTAT 1970		GCCAGGACCA 1990		TGGGTAGACAGCCAGGCCCCTGGCGCTGGACCCTGAGCTGGCGG 1980 1990 2000 2010 2020	 AGCTGGCGG 2020
Hum.	2000 GCATCCCCGGGAGC	2010 GGAGCATGTGA	0 2020 2030 2040 2050 2060 ATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCA	2030 GACCAGGGTC	2040 AGTGGTGGG	2050 cccccreec	2060 TGCCCAGCA
Mur.	:::: :::::::::::::::::::::::::::::::::	:::::: TGAGCGTGTGC 2040	::::: AGGTCCCGC 2050	:::::::: GACCAGGGTC 2060	::::::::::::::::::::::::::::::::::::::	: :::: CTTCCATGGC 2080	:::::::: TGGCTGCCCAGCG 2090
Ë	2070	2080	0 2120 2130 2130 2130 2120 2130 CHTTLO 2120 2130	2100	2110	2120	2130
Mur.	GTCCTACTGGCCCCA						CICAICAIC CICACICIC
	2100		2120	2130	2140	2150	2160
	2140	2150	2160	2170	2180	2190	2200
Hum.	GTGGCC	CCCCATTGAGA	TTGAGAGCACTCCGGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTG	CTCGGGGCAA	GGTTCAGGGC	TGTGAGACCC	TGCGCCCTG
Mur.	CGCT	TCCCCACTGGGG	TGCGGG	CTCGGGGTAA	GGTTCAGGGC	TGTGGGATGC	CTGCCCCCA
	2170	2180	2190	2200	2210	2220	2230

Fig. 27P

	2210 2220 GGGAGAAGGCCCCGTT ::::::::::::::::::::::::::::::		2230 ::::::::::::::::::::::::::::::::::	2230 2240 2250 2260 AGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGAC ::::::::::::::::::::::::::::::::	2250 ::::::: CTCCAAGGAC 2280 2320 TAAACTCTAG ::::: TAAACA-GGG 2350 2350 CAGCCCTGAC ::: CAGCCCTGAC	2230	2270 ACCTCTGCCAGTGA ::::::::::::::::::::::::::::::::::
_	AGACCACCITICICCC	2430 TCTCCCCTGAG	2440 BAGGAGCTTC	Z45U TGCTACTCTG	ZATCACTGAT	430 Z440 Z480 CTGAGAGGAGCTTCTGCTACTCTGCATGATGACACTCAGCAGGGTGATGC	Z480 GGGTGATGC
•• ()	::::: -GACCA	:: GGGT	:.::::: GGTAGGAGGC	:: :: :: :: :: :: :: :: :: :: :: :: ::	: :: .: CTA-ACGTGT(: ::

Fig. 27Q

COFFER CHEST

2490 2500 2550 2550 2550 2550 2550 2550 Hum. ACAGCAGTCTCCCCTATGGGACTCCCTTCTACCAAGCACTCTTAACAGGGTGGGGGCTTCTTACCAAGCACTCTTTTTTTT	2560 2570 2580 2600 2610 ACCCCCAGACCTGCTCCTACACTGATA-TTGAAGAACCTGGAGGATCCTTCAGTTCTGGCCATTCCAG . : :: ::: .: ::: .: .: .: .: .: .: .: .	2620 2630 2640 2650 2660 2670 2680 Hum. GGACCCT-CCAGAAACACA-GTGTTTCAAGAGATCCTAAAAAAACCTGCCTGTCCCAGGACCCTATGGTA :::::::::::::::::::::::::::::::::::	2690 2710 2720 2730 2740 2750 Hum. ATGAACACCAAACATCTAAACAATCATATGCTAA-CATGCCACTCCTGGAAACT-CCACTCTGAA : .::: ::::::::::::::::::::::::::::::
250 2510 2520 25 Hum. ACAGCAGTCTG-CCTCCCCTATGGGACTCCCTTCTACCAAGCACATGA :: ::: ::::::::::::::::::::::::::::::	2560 2570 Hum. ACCCCCAGACCTGCTCCTACACTGA: .:::::::::::::::::::::::::::::::::::	2620 2630 2640 Hum. GGACCCT-CCAGAAACACA-GTGTT ::::::::::::::::::::::::::::::::	2690 2700 2710 Hum. ATGAACACCAAACATCTAAACAATCATA' : .::: :::::::::::::::::::::::::::::::

Fig. 27R

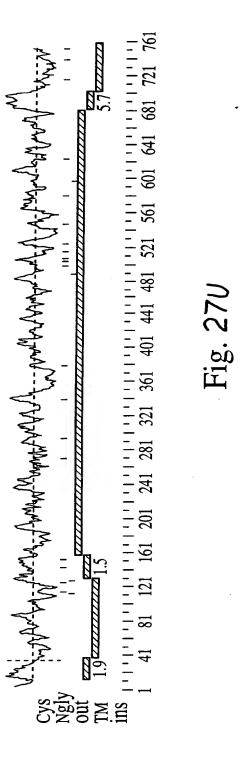
Hum.	2760 2770 2780 2790 2800 2810GCTGCCGCTTTGGACACCACCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCTGC
Mur.	::::::::::::::::::::::::::::::::::::::
Hum.	2820 2830 2840 2850 2860 2870 2880 TTCCCTTACCAGGCACCCTGCAGGAAGTCTTTCCTGAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
Mur.	TICCITIACCAGICGGCCATACTGITI 2800 2810 282
Hum.	2890 2900 2910 2920 2930 2940 2950 . TTCAGTTGGGGGCAGACTCTGAGCCTTCTTC
Mur.	::::::::::::::::::::::::::::::::::::::
Hum.	2960 3010 2980 2990 3000 3010 ACTCCTTTACCCTAGCTGACCCCTTCACCACCTCCCTTTCCTTT
Mur.	::: .:: CCTTGTCCAG 2930 29

Fig. 27S

Hum.		3030 GTCAGAGA	3040 CTGTTTAT	3020 3030 3040 3050 3060 3070 3080 AAACTGCTTGTCAGAGACTGTTTATTTTTTTTAAAAATATATAAGGCTTAAAAAAAA	3060 TATAAGGCTI	3070 TAAAAAAAA	3080 AAAAAAAAAAA
							•••••••••••••••••••••••••••••••••••••••
Mur.	AAACTGCTI	GTCACAGA	CAATTTAT	AAACTGCTTGTCACAGACAATTTATTTTTTTAAAAA			AGATATAA
	3000		3010	3020			3030

3090 3100 Hum. AAAAAAAGGGCGGCCGC

Mur. GCTTTAAAG---



OCZECETO CHEEL

				339/36	1			
79	6 150	26 210	46	930 330	86 390	106 450	126 510	146 570
AGGA	ု ည	I ATT	G GGA	E GAG	S AGT	L CTA	V GTT	M ATG
TCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCCAACTAAAGGA	T I ACA AT(T ACC	A GCT	S TCT	I ATC	A GCG	FLL	E GAA
SCAAC	K 1 AAG AC	Q CAG	Q CAA	G GGT	K AAA	K AAA	$_{ m CTT}$	N AAT
4AGG(T FACA A	S	V GTT	S AGC	I ATA	I ATC	P CCA	L TTA
CICCA	C 7 TGT A(S	G GGT	$_{ m ITA}$	N AAT	G GGA	S TCT	N AAC
PAACO	ניז	S TCA	Y TAT	D GAT	S TCA	V GTG	E GAG	K AAG
GACI		V GTC	D GAC	P CCA	F TTT	G GGA	F	$_{ m TTA}$
CCTI	AGG7	Y TAT	$_{ m L}$	L	N AAT	P	GGG	I ATT
GAC	CTGC	CIC	A GCA	K AAA	Y TAC	V GTG	W TGG	P
TGAG	CTGGATCTAGCTCCTGCAGGAG	N AAT	R AGG	K AAG	N AAC	FTT	D GAC	K AAA
TGCI	TCTF	W TGG	Q CAG	E GAA	V GTA	A GCT	T ACA	E GAG
CCTC	TGG	L CTG	T ACT	K AAA	Y TAT	$_{ m L}$	S AGC	M ATG
		L	I ATT	L CTA	D GAT	S TCA	I ATC	P
GGAC	AGA1	I TIC	R AGG	M ATG	V GTT	T ACC	N AAC	E GAG
CTT	;CAG	C TGT	A GCA	Q CAA	K AAA	N AAT	A GCC	A GCT
GCAG	ACAG	G GGA	K AAG	E GAG	L CTA	P CCA	T ACT	FTTT
GICC	CAGC	W TGG	I ATC	I ATT	F TTT	F TTT	GGC	S
ACGC	ວວອອາ	L	G GGA	M ATG	E GAA	S TCA	H CAT	N AAC
GTCGACCCACGCGTCCGCAGCTTTGGACACT	TCAAGAAAGGCCCAGCACAGCAGAAGATCAG	V GTC	P CCT	K AAG	L CTT	FTT	N AAC	Y TAT
GTCG	TCAA	P CCA	Y TAC	M ATG	S TCT	A GCC	T ACC	CIG

Fig. 28A

326 1110 166 186 206 226 810 266 630 069 286 990 306 L CTC G GGG Q CAA E GAA L CTC M ATG L CTG M ATG PCCA N AAC A GCT FITC T ACC S TCT E GAA S TCC T ACA N AAC P F ACA S TCT ഥ AGC S AGT $_{
m CTG}$ N AAC F TTC Q CAA Q CAG N AAT \gt LCIC I ATC S AGC 998 H CAT S TCC P CCA GTT \gt ⊢ AAC L CTA R CGC S TCC YTAC A GCT F TTT L ITG P CCA AAC A GCC $_{
m TTC}$ E GAA F TTT CAT I ATC Q CAA S TCC 工 Z K AAG V GTA PCCA Y TAC L CTA N AAT Y TAC S TCC N AAC CTA A GCG TCC I ATC D GAT LCTC N AÀT GGT Д ഗ K AAG E GAG ATC Q CAA L CTG V GTG ATT S TCT E GAG GCA ATA AAA L CTG L TTG F TTT K AAA Ø CCC L CTC N AAC E GAA I ATT TACT PCCT F TTT R CGG M ATG GAA Y TAC L CTG T ACC GTT $_{
m F}$ PCCT E GAG M ATG S AGT N AAC D GAC P CCA Y TAT S TCC S TCC I ATC E GAG GCA GAC LCTT S TCA L LCTC ACA \Box Н A GCC S TCC I ATT Y TAC F TTC A GCC T ACT V GTG K AAG N AAC PCCC I ATC L N AAC M ATG A GCC I ATT PCCC EGAG I ATC PCCT T ACC PCCC GGA N AAT G GGC R AGG I ATC D GAC I ATT F TTC LCTT T ACT V GTG D GAC T ACC Y TAC 9 9 I ATT V GTT V GTT

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28B Fig.

GAA

GTT

ACA

CCC

ACC

				341/301		
346 1170	366 1230	386 1290	406 1350	426 1410	446 1470	456 1500
L CIG	N AAC	P	F	Y TAT	S AGC	
R AGA	S AGC	L CTC	L TTA	K AAG	I ATA	
Q CAA	R CGC	V GTC	F TTC	L CTG	$_{ m L}$	
G GGA	N AAT	G GGA	K AAA	D GAC	N AAC	
L TTG	S TCC	F TTT	H CAC	T ACC	L CTG	
I ATT	E GAG	H CAC	P CCA	S TCC	G	
V GTT	P CCA	L	N AAT	I ATT	E GAA	
L	$_{ m L}$	I ATT	P	$_{ m ITG}$	W TGG	
9	A GCT	S TCC	L CTG	L	V GTA	
V GTT	CIT	s TCG	P CCT	F	H CAC	
S AGT	R CGC	L CTA	F TTT	G GGT	F	* TGA
T ACC	F	I ATT	G GGA	E GAG	S AGT	P CCT
S AGT	R AGA	N AAT	Q CAA	L	P CCA	A GCC
A GCT	N AAC	E GAA	Q CAG	V GTT	Q CAG	S TCA
V GTT	L	F TTT	$_{ m ITG}$	E GAA	Q CAG	K AAG
FTTC	S TCT	R AGG	K AAA	I ATT	K AAG	GGG
D GAC	$_{ m L}$	$_{ m L}$	A GCA	D GAT	S TCA	R AGG
M ATG	S TCC	V GTC	N AAT	S TCA	S TCC	W TGG
S	C TGC	E GAG	A GCC	N AAT	T ACA	Q CAG
V GTT	V GTC	I ATT	L CTG	V GTC	E GAA	R AGA

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1658 TIGCCGGITIGCAATICACCCCAGGAAGTAAATGGTCCTTAATCCTACAACTACTGTAAAACCCAGAAGGGAAAGACAGT TITGITIGITIGGGGCAAGAAGAITCIAGGACAAGAGCIAGGCAIGIACTICIGACCAGGIGGGIAAGCAACTCIAAG

COTTOLTO CLINOL

1895	1974	1980
TCTGTATTTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTCCCCTACCTGCATATTGGTTTTC	ATGTTTTATATTCACTGTTACTATCTTCTGTGTTTAATTAA	292299

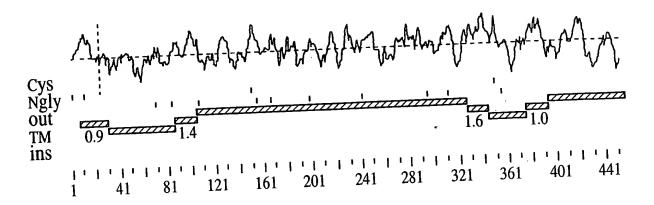


Fig. 28E

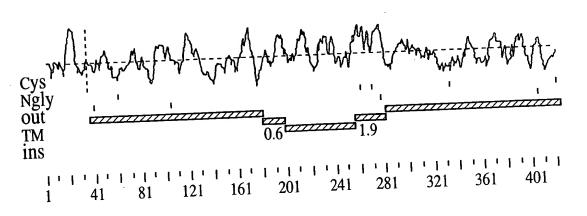


Fig. 29F

10 20 30 40 50 60 286 MCTKT-IPVLWGCFL-LWNLYVSSSQTIYPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLSGSESL : : : : : : : : : : : : : : : : : : :	90 100 110 130 ISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME : .: .: .: .: .: .: .: .: .: .: .: .: .:	140 150	··· · · · · · · · · · · · · · · · · ·	SISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHAALESALIMENS 200 140 150 160 170 170	160 170 180 200 210 220 286 VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSPVPFVLPERSN : .: .: .: .: .: .: .: .: .: .: .: .: .:
10 20 IPVLWGCFL-LWNLYVSSSQ 	70 80 90 286 EFLKVDYVNYNFSNIKISAFSFPNTS 		KPI	LKLGSNPTSGKPTITCSSCS 150 160	60 NANLSTLEVLTKIDNYTLLD
286 MCTKT- : BPI MARGPC	70 286 EFLKVC BPI KIKHLG		786	BPI SISAD	1 286 VKA-L : : : BPI VSSKL 210

Fig. 28F

24 YFFKSAS :::.:. YFFNTAG 290 :::: PTGLTFY 360 360 SFENILS CLQDIMN 430	440 450 286 QQPSFHVWEGLNLISRQWRGKSAP	BPI
---	---	-----

Fig. 28C

COVEDIO CHEPT

286 RENP 286	MCTKTIPV : MGALARAL 70 EFLKVDYV		20 60 MNLYVSSSQTIYPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLSGSE. : ::::::::::::::::::::::::::::::::::	30 YPGIKARITÇ SANPGLVARITI 30 100 LAFVPGVGIKAI	30 40 PGIKARITQRALDYGVQAGMI:: :::::::: PGLVARITDKGLQYAAQEGLI 30 40 100 110 VPGVGIKALTNHGTANISTDU	50 VQAGMKMIEQMLKE: AQEGLLALQSELLR 50 120 NISTDWGFESPLFV	WNLYVSSSQTIYPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLSGSESL : .: .: .: .: .: .: .: .: .: .: .: .: .:
RENP	RIPHVGRGRYEFHSL 70 80	XYEFHSLNJ 80	IHEFQLPSSQIS	MVPNVGLKFS	ISNANIKISG 110	KWKAQKRFLKI 120	NIHEFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGM 90 100 110 120
286	 	KI				140 EKN-LN]	140 LKN-LNEMLCPIIASE · · · ·
RENP		SSNPTSGKI 150	r. PTITCSSCSSHI 160	NSVHVHISKS 170	KVGWLIQLFHI 180	 KKIESALRNKI 190	\$Q 2
286	160 VKA-LNANI	170 LSTLEVLTK) KIDNYTLLDYSI	190 ISSPEITENY	200 LDLNLKGVFY	210 PLENLTDPPF	160 170 180 190 200 210 220 VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSPVPFVLPERSN
RENP		. :: :::: FQTLPVMTF 220	::::. TKIDSVAGINYGI 230	: .VAPPATTAET 240		SENHHNPPPF	: . : : : : : : : :

Fig. 28H

	230 240 250 260 270 280 290
286 RENP	SMLYIGIAEYFFKSASFAHFTAGVFNLTLSTEEISNHFVQNSQGLGNVLSRIAEIYILSQPFMV ::::::::::::::::::::::::::::::::::::
286 RENP	300 340 350 360 TEPPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTSVGLVILGQRLVCSLSLNRFRLALPE :::::.::::::::::::::::::::::::::::
286 RENP	370 380 400 410 420 430 SNRSNIEVLRFENILSSILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEVLEGFLLISTDLKYETSSK :: : : : : : : : : : : : : : :
286	440 450 QQPSFHVWEGLNLISRQWRGKSAP
RENP	

Fig. 281

79

∞	149	28	209	48	269
Ø	CAG	Ø	CAG	Z	
~	AGA (ഥ	TTC	F M	ATG
ഗ		Σ	ATG		
		≻		A	GCA
I L	ACC	A	909	떠	GAA
ᅜ	GAA	>	GTG	വ	\mathcal{O}
니	TTG	ы		Ω	
Σ	ATG	Н		>	
		Ы	CTG	A	GCT
	TGG.	Ы	CTT	\bowtie	AAA
	3ATG1	M		⊢	ACT
	AATGCAGATGTTGGACC	되 교	ATG	Д	CCA
	[AAA]	Œ	GAA	Σ	ATG
	AAAA	Σ	AGA ATG	Η	CAT
	3GAA/	~	AGA	>	TCA GTA CAT
	3GCA(Н	CAC	ഗ	TCA
	CATT	ഗ	TCA	Z	AAT
	ATTAGTTGCATTGGCAGGAAAAATA	>	GTC TCA CAC	>	AGA AAT GTG AAT
	\GTT(н	TGG ATT	R	AAT
	ATT?	M	TGG	ĸ	AGA

89 329 88 389 GAA T ACA ഥ ACT K AAG GCA K AAG GIC PCCT GAA Q CAA 回 Y TAT V GTG GAA L CTA E GAG 9 96C $_{
m TGT}$ R CGA PCCC P $^{
m Y}$ I ATT 9 99 9 R AGG AAC Q CAA Z H CAT V GTT Q CAA S TCT I ATC L I ATC I ATC E GAA Y TAT S AGT GGG I ATT D GAT

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449 108 I ATT W TGG N AAC s AGC A GCT GGT GGA V GTT L CTA . 960 H CAT Q CAG L CTG L TTA V GTG V GTG PCCT R AGG S TCC GGT

128 509 WV GTG D GAC FTTT GGT A GCT D GAT A GCA L CTG I ATT F TTC GGC $_{
m L}$ S AGC N AAT N AAC P $_{
m L}$ N AAC S TCC

148 Q CAA S TCC L CTC T ACA K AAG H. CAC K AAA R CGA S TCT \overline{W} A GCC N AAC GGA R AGG S AGC N AAC GGG G M ATG

Fig. 29A

				349/361				
168	188	208	228	248	268	288	308	328
629	689	749	809	869	929	989	1049	1109
I	g	M	F	Q	I	R	W	N
ATA	GGC	ATG	TTT	CAG	ATT	CGA	TGG	AAT
V	Q	K	K	$_{\mathtt{TAT}}^{\mathtt{Y}}$	Q	S	H	K
GTG	CAG	AAA	AAA		CAG	AGC	CAC	AAA
A GCA	S TCA	I ATC	TACC	L	D GAT	M ATG	L CTA	T ACC
PCCT	YTAT	K AAA	999	F TTT	L	N AAC	I ATT	E GAG
L	ე <u>ე</u> ნე	Q CAG	P	E GAA	I ATT	M ATG	N AAT	S AGT
D	V	A	S	K	V	N	Q	GGG
GAC	GTC	GCT	AGC	AAA	GTG	AAT	CAA	
표 대 대 대	m Y TAT	L	K AAA	K AAA	Q CAG	N AAC	V GTG	W TGG
R	Y	E	A	9		T	S	D
AGG	TAT	GAG	GCA	9	9	ACC	TCT	GAC
A	I	P	H	F	C	N	T	F
GCT	ATC	CCA	CAT	TTT	TGT	AAC	ACA	TTT
M ATG	K AAG	M ATG	K AAG	$_{ m L}$	L	F TTC	G	A GCA
E	E	TACC	V	G	Y	G	A	R
GAG	GAA		GTT	GGA	TAC	GGA	GCT	CGG
D GAT	Q CAG	S TCC	TACT	K AAG	I ATT	G	L	L
Y	9	F	A	I	V	L	T	E
TAT	9	TTT	GCC	ATC	GTT		ACT	GAA
S AGT	TACG	A GCA	I ATA	MATG	L	L	H CAC	G
F	K	I	P	M	Q	L	A	S
TTC	AAA	ATT		ATG	CAA	TTA	GCC	TCT
A	Q	F	A	D	R	M	A	N
GCT	CAG	TTT	GCA	GAT	AGA	ATG	GCT	AAT
W TGG	$_{ m L}$	9 9	L TTA	P CCA	CIC	I ATC	Y TAT	V GTG
F	I	M	A	L	${ m F}$	N	V	A
TTC	ATT	ATG	GCT	CTG		AAT	GTA	GCA
E GAG	F TTT	TACC	F TTT	$_{ m L}$	R AGA	S AGT	S AGT	Q CAG
D	N	T	Y	$_{ m TTG}$	T	C	A	S
GAT	AAC	ACC	TAT		ACC	TGT	GCA	AGC

Fig. 29B

348	368	388	408	424
1169	1229		1349	1397
PCCT	L	D GAT	Q CAG	
V	M	V	M	
GTC	ATG	GTG	ATG	
T ACG	K AAA	H CAC	L	
M	V	A	H	
ATG	GTG	GCT	CAT	
D	D	\overline{W}	I	*
GAT	GAC		ATC	TGA
R	E	. E	I	$_{ m ITG}$
AGA	GAA	GAA	ATC	
V	P	P	E	V
GTC	CCA	CCT	GAA	GTA
R	N	I	N	A
AGA	AAT	ATT	AAT	GCC
$^{ m Y}$	S	N	Y	E
	TCA	AAT	TAC	GAG
R AGG	L	K AAG	M ATG	$_{\rm TGT}^{\rm C}$
V	W	H	R	R
GTA	TGG	CAT	CGT	CGG
P	D	Y	H	G
CCT	GAC	TAC	CAC	GGA
TACT	Q CAG	I ATC	PCCT	Q CAG
P CCA	GGT	L	A GCT	S TCC
Q	G	N	D	L
CAG	GGA	AAC	GAT	CTT
N	T	T	$_{ m ITG}$	N
AAT	ACA	ACC		AAC
C	W	V	G	T
TGC	TGG	GTG	GGT	ACC
K	M	E	W	E
AAA	ATG	GAG	TGG	GAG
E	A	S	I	E
GAA	GCA	TCT	ATC	GAG
L CTG	T ACA	L	FTTC	O CAG

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1476 1792 1950 2029 1871 AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGGCTAGGACCCATGAAGGCAGAATTACGGAGAGACA TTAAAGTACTTATTAGGTAAATAGAGGTTTTTGTATGCTATTATATATTCTACCATCTTGAAGGGTAGGTTTTACCTGAT ATTTTTGGAGCACTAAAGTAAAATGGCAAATTGGGACAGATATTGAGGTCTGGAGTCTGTGGATTATTGTTGACTTTGA CAAAATAAGCTAGACATTTTCACCTTGTTGCCACAGAGACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA CAACAACAAAATCAGTGTTACAGTATGGATGAAATCTATGTTAAGCATTCTCAGAATAAGGCCAAGTTTTATAGTTGCA AAAAAGGGCGGCCGC

Fig. 29(

10 20 30 40 50 60 70 294 MLETLSRQWIVSHRMEMWLLILVAYMFORNVNSVHMPTKAVDPEAFMNISEIIQHQGYPCEFYEVATEDG : : : : : : : : : : : : : : : : : : :

Fig. 29D

280	290	300	310	320	330	340	
294 NTNNMNN	1SRASVYAAHT	LAGTSVQNIL	HWSQAVNSGE.	LRAFDWGSET	KNLEKCNQPI	294 NTNNMNMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVPT	
HLP DSKNFNTSRLDVYLSH	SKNFNTSRLDVYLSHN	::::::: IPAGTSVQNMF	:::::: HWTQAVKSGK	:.::. FQAYDWGSPV	.: ·QNRMHYDQS(. ::::::::::::::::::::::::::::::::::::	
270	280	290	300	310	320	330	
350	360	370	380	390	400	410	
294 AMWIGGQDWLSNPEDV	DWLSNPEDVK	MLLSEVTNLI	YHKNI PEWAH'	VDFIWGLDAE	HRMYNEIIHI	KMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGRC	
HLP AVWNGGP	HLP AVWNGGKULLADPQUVGLLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVINDIVSMISEDKK- 340 350 360 370 370 380	JUPKLPNLI 360	XHKELPFYNH. 370	LDFTWAMDAE 380	70EV YND1VSIV 390	A L S E D K K	
420							
294 EAVL							
HLP							

Fig. 29E

60 GYPCEEYEVATE :::::::: GFPSEEYLVETE 50	130 WMGNSRGNAWS :::::::: WMGNSRGNTWS	200 TMPELAQKIKM .:::::: QIPELAKRIKM 190	270 ICSNIMLLLGG .:.:.::: LCGNLCFLLCG 260
20 30 40 50 60 EMWLLILVAYMFQRNVNSVHMPTKAVDPEAFMNISEIIQHQGYPCEEYEVATE :: :: :: :: :: :: :: :: :: :: :: :: ::	70 80 100 100 130 DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNAWS ::::::::::::::::::::::::::::::::::::	160 170 180 190 200 FSYDEMARFDLPAVINFILQKTGQEKIYYVGYSQGTTMGFIAFSTMPELAQKIKM :::::::::::::::::::::::::::::::::::	230 240 250 260 270 PGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLLGG : .: .: .: .: .: .: .: .: .: .: .: .: .:
40 1PTKAVDPEA 1 :::: SGGKLTAVDPET 30	110 ASNWISNLPNNS :::::	180 <tgqekiyyvg> ::::::::: <tgqeqvyyvg> 170</tgqeqvyyvg></tgqekiyyvg>	250 SFLYQTRFLRQI :::::::: SFLPQSAFLKWI
30 MFQRNVNSVHN 	100 VLLQHGLVGGZ :.::::::: VFLQHGLLADS	170)LPAVINFILQE ::: :::::)LPASINFILNE 160	240 NMMIKGLFGKKF .::.::
20 MEMWLLILVAYM: ::KMRFLGLVVCL ¹ 10	90 .VQPKKTGSRP\ . :: KKNHSDKGPKP\	160 ARESYDEMARFDLPAN :::::::::: RAFSYDEMAKYDLPAS 150	230 240 SSPGTKFLLLPDMMIKGLFGK :: .: .: .: .: .: .: .: .: .: .: .: .: .
10 MLETLSRQWIVSHRM : M	70 80 DGYILSVNRIPRGLV ::::: .:::: DGYILCLNRIPHGRK 60 70	140 150 294 RKHKTLSIDQDEFWA :::::::::::: LAL RKHKTLSVSQDEFWA 130 140	10 220 YFALAPIATVKHAKS .:::.::::::::::::::::::::::::::::::::
294 ML: : LAL M-	70 294 DG :: LAL DG	140 294 RKJ :: LAL RKJ	210 294 YF: .: LAL FF: 2

Fig. 29G

- •	280	290	300	310	320	330	340
294	FNTNNMNI	MSRASVYAAHT	LAGTSVQNIL	HWSQAVNSGEI	RAFDWGSETK	NLEKCNOPTE	294 FNTNNMNMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVP
LAL	FNERNIN		PAGTSVQNML	:::::: HWSQAVKFQKF	 QAFDWGSSAK	: ::::::::::::::::::::::::::::::::::::	LAL FNERNLNMSRVDVYTTHSPAGTSVQNMLHWSQAVKFQKFQAFDWGSSAKNYFHYNQSYPPTYNVKDMLVP
	270	280	290	300	310	320	330
•	350	360	370	380	390	400	410
294	TAMWTGG	2DWLSNPEDVK	MLLSEVTNLI	YHKNIPEWAHV	'DFIWGLDAPH	RMYNE I IHLN	294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
	••••••	•	•		•••		
LAL	TAVWSGG	LAL TAVWSGGHDWLADVYDVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKIINLMRKYQ	ILLTQITNLV	FHESIPEWEHI	DFIWGLDAPW	RLYNKIINLN	4RKYQ
	340	350	360	370	380	390	
*	420						
294	294 CEAVL						
LAL	 - -						

Fig. 29H

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2 75	22	42 195	62 255	82 315	102 375	122 435	142 495	162 555
s E	T ACC	$_{ m CTG}$	FTTC	S AGC	Q CAG	E GAG	C TGT	T ACT
M S ATG GCT	D GAC	I ATC	L TTA	V GTC	L	N AAT	E GAG	F TTC
	M ATG	V GTC	S AGC	Q CAG		L CIG	E GAG	K AAG
CCAA	P CCG	I ATC	T ACC	9 990	I ATT	Q CAG	A GCT	E GAG
CTCA	F TTC	F TTC	V GTG	V GTG	D GAT	Q CAG	YTAT	A GCT
CCAC	ACC	T ACG	V GTG	S TCT	A GCT	V GTG	N AAC	L CTA
TGCA	P CCA	A GCC	R CGG	W TGG	S AGC	CCC	E GAG	Y TAC
SGGGCGCAGCATTGCCCCCCCTGCACCACCTCACCAAG	K AAG	L CTG	L	E GAG	I ATC	T ACC	G GGT	$_{ m L}$
	р ССС	A GCA	L CTG	S TCT	₩ TGG	GGG	L CTG	V GTG
CATI	9 9	T ACT	\overline{W}	S AGT	E GAG	T ACA	R CGC	P
GCAG	A GCT	Γ	F	F TTC	S TCT	L	W TGG	D GAC
99999	Y TAT	F TTT	L CTG	N AAT	S AGT	T ACA	T ACC	P CCA
	F	I ATC	R AGG	V GTG	H H C	I ATC	FITC	LCTG
3GGC1	P	M ATG	T ACG	A GCT	A GCC	N AAC	E GAG	GGG
SCGAC	F TTC	I ATC	K AAG	L CIG	K AAG	V GTC	E GAG	K AAG
CACGC	TACA	I ATC	G GGA	I ATC	Y TAC	G GGA	N AAC	E GAG
GTCC	H CAC	S AGC	R CGG	A GCA	S TCA	G GGT	Y TAC	L CTG
ACGC	G GGA	A GCC	I ATT	A GCT	T ACA	L CTG	N AAT	A GCT
GTCGACCCACGCGTCCACGGCGAGGGCTCCC	$_{ m L}$	$_{ m L}$	GGC	ტ ტტტ	N AAC	GGG	I ATC	K AAG
GTCC	T ACT	T ACT	P CCT	I ATC	TACC	V GTC	TACC	A GCA

Fig. 30A

356/361 202 675 242 795 262 282 915 302 975 322 V GTG A GCC LCTC V GTG FTTC LCTC ഗ L CTG P CCT S TCT GGA CTGT ⋖ G ACC M ATG L CTG K AAG A GCT A GCT GGT PCCC G S TCC GGC L CTG $_{\rm L}$ GAA 口 CAC $_{
m L}$ L CTG GGA AGG GAG L CTC G α 되 \Box GGA Q CAG H CAC ACA H CAC Q CAG CCT Σ Ħ Д GCG GTG F TTC L CTG ACC CCT AGT \gt \vdash Д ഗ ഗ I ATC PCCC L TTG Q CAG TGG K AAG AAT z ⋈ CCC GGC ACA ATG GAG CGC $^{\rm C}$ Þ G \vdash $\mathbf{\Sigma}$ Œ Д Γ ACG P I ATC R AGG L CTG \vdash S CAG gccTGG ATG $_{
m L}$ S TCA H CAC Ø \geq Σ Ω R CGC TGG $_{
m ITG}$ TACC F TTC A GCC CCC A GCT \mathbb{Z} Д L CTA M ATG TAC IGC LCTC SCC GTG GAC Ö Ø \Box \gt M ATG A GCG GAA S TCC L CTC S TCA PCCT ഥ GGG M ATG R GGC Y TAC T ACA GAT FTTC G Ω \Box V GTG GCA G GGC A GCC H CAT A GCT YTAC ø M ATG CCA GTG H CAC L CTG S AGT R CGC GGT \gt Q CAG AGC ¥ TGG Y TAT S TCC TACT 9 9 P ഗ $_{
m L}$ AAC AGA L CTA GTA FTTC H CAT α \gt Z S M ATG Γ $_{
m L}$ F TTC Γ PCCA L CTG F TTC

30B Fig.

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⊱

GCT

GAT

CCI Д

GAT

AAA

CCC

CAC

GCA

GAG

AAG

TAC

 $^{\mathrm{C}}$

A GCA

K AAG

T ACC

S TCC

S TCC

E GAG

GCT Ø

AGC

 $^{\mathrm{C}}$

1035

TCA

GAC

TCC

CCC

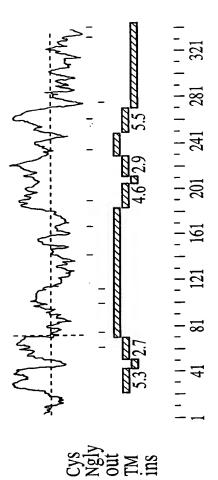
AGT

GAC

* ⊢	344
TTA TAA	1101
CATICCICCCCGIGGAGGCCACCIGGACTICCAGICIGGCICCAAACCICATIGGCGCCCCAIAAAACCAGCAGAACIG	1180
CCCTCAGGGTGGCTGTTACCAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAAAGGAGGCTCTATATACTGATGTT	1259
AAAAAACAAAACAAAACAAAAAGCCCTAAGGGACTGAAGAGATGCTGGGCCTGTCCATAAAGCCTGTTGCCATGATAAG 1338	1338
GCCAAGCAGGGGCTAGCTTATCTGCACAACCCAGCCTTTCCGTGCTGCCTTGCCTTCAAGATGCTATTCACTGA 1417	1417
AACCTAACTTCACCCCCATAACACCAGCAGGGTGGGGGTTACATATGATTCTCCTATGGTTTCCTCTCATCCTCGGCA 1496	1496
CCTCTTGTTTTCCTTTTTCCTGGGTTCCTTTTGTTCTTCCTTTACTTCTCCAGCTTGTGTGGCCTTTTGGTACAATGAA 1575	1575
AGACAGCACTGGAAAGGAGGGGAAACCAAACTTCTCATCCTAGGTCTAACATTAACCAACTATGCCACATTCTCTTTGA 1654	1654
GCTICAGIICCCAAAITIGCIACAIAAGAIIGCAAGACIIGCCAAGAAICIIGGGAIITIAICIIICIAIGCCIIGCIGA 1733	1733
CACCTACCTTGGCCCTCAAACACCCCTCACAAGAAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAACGCTATTCCT 1812	1812
TCCCACCCCACTCAGCTGGGCTAGCTGGCATCCAGGACGGGGGAGTGGGTGACCTGCCTCATCACTGCCACCTAA	1891
CGTCCCCCTGGGGTGGTTCAGAAAGATGCTAGCTCTGGTAGGGTCCCTCCGGCCTCACTAGAGGGCGCCCCTATTACTC	1970
TGGAGTCGACGCAGAGAATCAGGTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCCAGCGAAGCTCATGA 2049	2049
GGACGTGCGACCCCGGCGCGGAGAAGCCATGAAAATTAATGGGAAAAAAAA	2128
25225	2133

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Fig. 30C



70	AAILAV	.:: GALIAS		130	NEEFIW		NEGFDI	
09	VTSLFIG	: : : : : : : : : : : : : : : : : : :	50		IETINYI	•••	DMTELYY	120
50	rrlewllr\	SIFSVFLIPLIAYILILPGVR-RKRVVTTVTYVLMLAVGGALI	40	120	IGTPVQQL N		SSNDVLPGS	110
	[LPGIRGK]	:::::: LLPGVR-RF	30		[L]		LKFERLLS	100
40	ALATFIVI	.::. PLIAYIL]		110	GIGGVNIT	::	GLQKVNVJ	06
30	PTFPMDTTLASIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLFIGAAILAV	::::.:::::::::::::::::::::::::::::::	20	100	SADIGLQV		QFRGHSNERILAKIGVEIGLQKVNVTLKFERLLSSNDVLPGSDMTELYYNEGFDI	σ
20	FPMDTTLA	IN5		06	KAFSSEWI	•••••••••••••••••••••••••••••••••••••••	RGHSNERI	80
0	FYAGPKPT	 ASSR	10	0	QVSTNTSY	•	SOMIYTOF	7.0
10	296 MATLGHTFPFYAGPK	:: CRP M-RIAH		80	296 NFSSEWSVGQVSTNTSYKAFSSEWISADIGLQVGLGGVNITLTGTPVQQLNETINYNEEFTW	••	CRP LIYPCWASGSQMIYT	09
	296 M	: CRP M			296 N		CRP L	

Fig. 30E

200	NV-MLSM	::	VVLMLFL	0	260	TGLLCVL	•••	IGITCVL	260
190	AFLCWLLA	•••••	AFACWCLS	190		WITLT	•	FCFYLIFA	250
180	HYTSAMLWV		HYTHAAIWE	180	250	FQLLALLFFSMATSLTSPCPLHLGASVLHTHHGPAFWITLTTGLLCVL	••••••	SCLIACLVYLLLSPCELRIAFTGENFERVDLTATFSFCFYLIFAIGILCVL	240
170	LYRQYRLAG	•••	WGRHYRVAG	170	240	LGASVI		IAFTGENFE	230
	FT-PRSPCG	•	FSTNODSFD	160	230	SLISPCPLH	••••••	-LLSPCELR	220
160	DPVLYLAEK	•••••••••••••••••••••••••••••••••••••••	YPMLSVLEY	150		ALLFESMAT	•	ACLVYL	2
150	KALEKGLP	•••	HGLENGLP	140	220	ATGIFQLL	•••	ATGISCLI	210
140	296 RLGENYAEECAKALEKGLPDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLANV-MLSM	::	CRP SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCLSVVLMLFL	130	210	296 PVLVYGGYMLLATGI	•	CRP PHNAYKSILATGI	200
	296 R		CRP S			296 P	••	CRP P	

Fig. 30F

320	296 LGLAMAVAHRMQPHRLKAFFNQSVDEDPMLEWSPEEGGLLSPRYRSMADSPKSQDIPLSEAS	•	CRP CGLGLGICEHWRIYTLSTFLDASLDEHVGPKWKKLPTGGPALQGVQIGAYGTNTTNSSRDKNDISSDKTA	330					
ĸ	SPKSQD.	•••	SRDKND	320					
310	-RSMAI	•	UNTINE			근		ST	
	LSPRY		DIGAYG	310		CAL	.:	SSASLRSQSSIETVHDEAELERTHVHFLQEPCSSSST	380
300	EGGLI		ILQGV					/HFLQI	
(')	SPE	:	PTGGP?	300				LERTH1	370
	EW	••	KWKKL		340	PKDPD	•	HDEAE	
290	3DPML		EHVGP!	290		EAHPKDPD		SIETV	360
5	1QSVDI	•	ASLD					RSOS	
30	KAFF	:	STFLI	280				ASSASI	350
280	1 QPHRI	•	RIYTI			-CK		COSSA	
0	VAHEN		CEHM	270				SRTSI	340
270	LGLAMA		CGLGLG		330	296 STKAYCK	:	CRP GSSGFQSRTSTCQSSA	
	296		CRP			296		CRP	

370 Fig. 30G